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/sex="female"
/cell type="hemocyte"
/tissue type="hemolymph"
/dev stage="adult"
/nc= "ASAP-UW Feature ID: 37052"
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/note="unknown; ASAP-UW Feature ID: 37053"

ORIGIN
Query Match 20.0%; Score 2; DB 3; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
  ||
Db 28 WG 27

RESULT 115
CNS000ARA
LOCUS
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR21022 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL055937
VERSION AL055937.1 GI:4936706
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 60)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammoler in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
P1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES
source
Location/Qualifiers
1. .60
/organism="Drosophila melanogaster"
/mol type="genomic DNA"
/db xref="taxon:7227"
/clone="BACR21022"
/clone_lib="RPCI-98"
/note="end : T7"

ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4
  ||
Db 37 RC 36

RESULT 117
CNS0101K
LOCUS
DEFINITION Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04H02 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION AL099014
VERSION AL099014.1 GI:5610625
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE 1 (bases 1 to 60)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

```

```

COMMENT      Determination of this BAC-end sequence was carried out as part of a
              collaboration with the European Drosophila Genome Project (EDGP) -
              http://www.edgp.ebi.ac.uk --. This Drosophila melanogaster BAC
              library (Dros BAC) was made by Alain Billaud at CEPH (Centre
              d'Etude du Polymorphisme Humain) with funding provided by a MRC
              project grant. The DNA was prepared from embryos by Alain Bucheton
              and Genevieve Payan. It has been constructed in the vector
              pBelobAC11.

FEATURES      source
              Location/Qualifiers
              1..60
              /organism="Drosophila melanogaster"
              /mol_type="genomic DNA"
              /db_xref="taxon:7227"
              /clone="BACN04H02"
              /clone_lib="DrosBAC"
              /plasmid="pBelobAC11"
              /note="end : T7"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WG 7
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      15 WG 16

Db

RESULT 118
CNS0101K/c
LOCUS
DEFINITION      Drosophila melanogaster genome survey sequence T7 end of BAC
BACN04H02 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL099014.1 GI:5610625
VERSION
KEYWORDS
SOURCE
ORGANISM      Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 60)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk --. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES      Location/Qualifiers
              1..60
              /organism="Drosophila melanogaster"
              /mol_type="genomic DNA"
              /db_xref="taxon:7227"
              /clone="BACN05H08"
              /clone_lib="DrosBAC"
              /plasmid="pBelobAC11"
              /note="end : T7"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WG 7
      ||
      58 WG 59

Db

RESULT 120
CNS0115W
LOCUS
DEFINITION      Drosophila melanogaster genome survey sequence T7 end of BAC
BACN05H08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL099854.1 GI:5611465
VERSION
KEYWORDS
SOURCE
ORGANISM      Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 60)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk --. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES      source
              Location/Qualifiers
              1..60
              /organism="Drosophila melanogaster"
              /mol_type="genomic DNA"
              /db_xref="taxon:7227"
              /clone="BACN04H02"
              /clone_lib="DrosBAC"
              /plasmid="pBelobAC11"
              /note="end : T7"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WG 7
      ||
      58 WG 59

Db

RESULT 120
CNS0115W/c
LOCUS
DEFINITION      Drosophila melanogaster genome survey sequence T7 end of BAC
BACN05H08 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION      AL099854.1 GI:5611465
VERSION
KEYWORDS
SOURCE
ORGANISM      Drosophila melanogaster (fruit fly)
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 60)
Genoscope.
Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk --. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES      source
              Location/Qualifiers
              1..60
              /organism="Drosophila melanogaster"
              /mol_type="genomic DNA"
              /db_xref="taxon:7227"
              /clone="BACN04H02"
              /clone_lib="DrosBAC"
              /plasmid="pBelobAC11"
              /note="end : T7"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CW 5
      ||

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http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaut at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelOBAC11.

FEATURES

source
1. .60
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN05H08"
/clone_lib="DrosBAC"
/plasmid="pBelOBAC11"
/note="end : T7"

ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
||
Db 59 CW 58

RESULT 121

CNS01TCC

LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 194D07 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION
AL166341
VERSION
AL166341.1 GI:7804079

KEYWORDS
GSS; genome survey sequence.

SOURCE

ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE
Estimate of human gene number provided by genome-wide analysis

JOURNAL
Nat. Genet. 25 (2), 235-238 (2000)

MEDLINE
20296633

PUBMED
10835645

REFERENCE

2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE
Characterization and repeat analysis of the compact genome of the

JOURNAL
freshwater pufferfish Tetraodon nigroviridis

MEDLINE
20359837

PUBMED
10899143

REFERENCE
3 (bases 1 to 60)

Genoscope.

Direct Submission

TITLE
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

JOURNAL
- Web : www.genoscope.cns.fr)

COMMENT
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

FEATURES

source
1. .60
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"

/db_xref="taxon:99883"

/clone="194D07"

/clone_lib="G"

/note="Genoscope sequence ID : COAG194CB04SP1-end : PUC-Ori"

ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
||
Db 53 CW 54

RESULT 122

CNS01TCC/c

LOCUS

DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 194D07 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION
AL166341

VERSION
AL166341.1 GI:7804079

KEYWORDS
GSS; genome survey sequence.

SOURCE

ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.

TITLE
Estimate of human gene number provided by genome-wide analysis

JOURNAL
using Tetraodon nigroviridis DNA sequence

MEDLINE
Nat. Genet. 25 (2), 235-238 (2000)

PUBMED
20296633

REFERENCE
10835645

REFERENCE

2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.

TITLE
Characterization and repeat analysis of the compact genome of the

JOURNAL
freshwater pufferfish Tetraodon nigroviridis

MEDLINE
Genome Res. 10 (7), 939-949 (2000)

PUBMED
20359837

REFERENCE
10899143

REFERENCE
3 (bases 1 to 60)

Genoscope.

Direct Submission

TITLE
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

JOURNAL
- Web : www.genoscope.cns.fr)

COMMENT
This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at http://www.genoscope.cns.fr/Tetraodon.

FEATURES

source

1. .60
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="194D07"
/clone_lib="G"
/note="Genoscope sequence ID : COAG194CB04SP1-end : PUC-Ori"

ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      4 CW 5
      ||
Db      55 CW 54

RESULT 123
CNS028B0
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
244D05 of library G from Tetraodon nigroviridis, genomic survey
sequence.
        60 bp      DNA      linear      GSS 01-SEP-2000
CNS028B0
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
244D05 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL185733
VERSION
AL185733.1 GI:7823837
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
ESTIMATE of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE
20296633
PUBMED
10835645
REFERENCE
2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
ESTIMATE of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE
20296633
PUBMED
10835645
REFERENCE
3
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL
Genome Res. 10 (7), 939-949 (2000)
MEDLINE
20359837
PUBMED
10899143
REFERENCE
3 (bases 1 to 60)
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
Location/Qualifiers
1..60
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="244D05"
/clone_lib="G"
/note="Genoscope sequence ID : COAG244CB03SP1-end :
PUC-Ori"
ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 WG 7
      ||
Db      36 WG 37

RESULT 124
CNS028B0/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
244D05 of library G from Tetraodon nigroviridis, genomic survey
sequence.
        60 bp      DNA      linear      GSS 01-SEP-2000
CNS028B0/c
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
244D05 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL201033
VERSION
AL201033.1 GI:7859378
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
ESTIMATE of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE
20296633
PUBMED
10835645
REFERENCE
2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
ESTIMATE of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE
20296633
PUBMED
10835645
REFERENCE
3
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL
Genome Res. 10 (7), 939-949 (2000)
MEDLINE
20359837
PUBMED
10899143
REFERENCE
3 (bases 1 to 60)
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
Location/Qualifiers
1..60
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="244D05"
/clone_lib="G"
/note="Genoscope sequence ID : COAG244CB03SP1-end :
PUC-Ori"
ORIGIN
Query Match 20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      6 WG 7
      ||
Db      36 WG 37

RESULT 125
CNS02K40
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
144B24 of library G from Tetraodon nigroviridis, genomic survey
sequence.
        60 bp      DNA      linear      GSS 01-SEP-2000
CNS02K40
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
144B24 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL201033
VERSION
AL201033.1 GI:7859378
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
ESTIMATE of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE
20296633
PUBMED
10835645
REFERENCE
2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
ESTIMATE of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE
20296633
PUBMED
10835645
REFERENCE
3
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL
Genome Res. 10 (7), 939-949 (2000)
MEDLINE
20359837
PUBMED
10899143
REFERENCE
3 (bases 1 to 60)
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
Location/Qualifiers
1..60
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/db_xref="taxon:99883"
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/note="Genoscope sequence ID : COAG244CB03SP1-end :
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      4 CW 5
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Db      37 CW 36

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Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A., Wincker,P., Brottier,P., Quetier,F.,
                Saurin,W. and Weissenbach,J.
TITLE        Estimate of human gene number provided by genome-wide analysis
                using Tetraodon nigroviridis DNA sequence
JOURNAL      Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE      20296633
PUBMED       10835645
REFERENCE
2
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A. and Weissenbach,J.
TITLE        Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetraodon nigroviridis
JOURNAL      Genome Res. 10 (7), 939-949 (2000)
MEDLINE      20359837
PUBMED       10899143
REFERENCE
3 (bases 1 to 60)
Genoscope.
Direct Submission
JOURNAL      Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
TITLE        This sequence is a single read and was generated as part of a large
                scale clone-end sequencing project of the Tetraodon nigroviridis
                genome. For more information, please take a look at
                http://www.genoscope.cns.fr/Tetraodon.
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PUC-Ori"
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 WG 7
      ||
Db      12 WG 13

RESULT 126
CNS02K40/C
LOCUS      CNS02K40
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            144B24 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION  AL201033
VERSION     AL201033.1 GI:7859378
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
ORGANISM    Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fischer,C.,
                Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                Saurin,W. and Weissenbach,J.
TITLE        Estimate of human gene number provided by genome-wide analysis
                using Tetraodon nigroviridis DNA sequence
JOURNAL      Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE      20296633
PUBMED       10835645
REFERENCE
2
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A. and Weissenbach,J.
TITLE        Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetraodon nigroviridis
JOURNAL      Genome Res. 10 (7), 939-949 (2000)
MEDLINE      20359837
PUBMED       10899143
REFERENCE
3 (bases 1 to 60)
Genoscope.
Direct Submission
JOURNAL      Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
TITLE        This sequence is a single read and was generated as part of a large
                scale clone-end sequencing project of the Tetraodon nigroviridis
                genome. For more information, please take a look at
                http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 WG 7
      ||
Db      12 WG 13

RESULT 127
CNS02O1W
LOCUS      CNS02O1W
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
            153N19 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION  AL206753
VERSION     AL206753.1 GI:7865572
KEYWORDS    GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis
ORGANISM    Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
            Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fischer,C.,
                Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                Saurin,W. and Weissenbach,J.
TITLE        Estimate of human gene number provided by genome-wide analysis
                using Tetraodon nigroviridis DNA sequence
JOURNAL      Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE      20296633
PUBMED       10835645
REFERENCE
2
AUTHORS      Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A. and Weissenbach,J.
TITLE        Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetraodon nigroviridis
JOURNAL      Genome Res. 10 (7), 939-949 (2000)
MEDLINE      20359837
PUBMED       10899143
REFERENCE
3 (bases 1 to 60)

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Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CW 5
        ||
DB      12 CW 13

RESULT 130
CNS0330M/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
208105 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION      AL225535
VERSION        AL225535.1 GI:7884433
KEYWORDS       GSS; genome survey sequence.
SOURCE         Tetraodon nigroviridis
ORGANISM       Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
1
AUTHORS        Roset Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                Saurin,W. and Weissenbach,J.
TITLE          Estimate of human gene number provided by genome-wide analysis
                using Tetraodon nigroviridis DNA sequence
JOURNAL        Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE        20296633
PUBMED         10835645
REFERENCE
2
AUTHORS        Roset Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A. and Weissenbach,J.
TITLE          Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetraodon nigroviridis
JOURNAL        Genome Res. 10 (7), 939-949 (2000)
MEDLINE        20359837
PUBMED         10899143
REFERENCE
3 (bases 1 to 60)
AUTHORS        Genoscope.
TITLE          Direct Submission
JOURNAL        Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT        This sequence is a single read and was generated as part of a large
                scale clone-end sequencing project of the Tetraodon nigroviridis
                genome. For more information, please take a look at
                http://www.genoscope.cns.fr/Tetraodon.
FEATURES       source
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WG 7
        ||
DB      13 WG 12

RESULT 131
CNS03C5T
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
013P19 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION      AL237386
VERSION        AL237386.1 GI:7896521
KEYWORDS       GSS; genome survey sequence.
SOURCE         Tetraodon nigroviridis
ORGANISM       Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
1
AUTHORS        Roset Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                Saurin,W. and Weissenbach,J.
TITLE          Estimate of human gene number provided by genome-wide analysis
                using Tetraodon nigroviridis DNA sequence
JOURNAL        Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE        20296633
PUBMED         10835645
REFERENCE
2
AUTHORS        Roset Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                Saurin,W., Bernot,A. and Weissenbach,J.
TITLE          Characterization and repeat analysis of the compact genome of the
                freshwater pufferfish Tetraodon nigroviridis
JOURNAL        Genome Res. 10 (7), 939-949 (2000)
MEDLINE        20359837
PUBMED         10899143
REFERENCE
3 (bases 1 to 60)
AUTHORS        Genoscope.
TITLE          Direct Submission
JOURNAL        Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
                BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
                - Web : www.genoscope.cns.fr)
COMMENT        This sequence is a single read and was generated as part of a large
                scale clone-end sequencing project of the Tetraodon nigroviridis
                genome. For more information, please take a look at
                http://www.genoscope.cns.fr/Tetraodon.
FEATURES       source
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RC 4
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DB      10 RC 11

RESULT 132
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LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
013P19 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION      AL237386
VERSION        AL237386.1 GI:7896521
KEYWORDS       GSS; genome survey sequence.
SOURCE         Tetraodon nigroviridis
ORGANISM       Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE AUTHORS

TITLE

Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence

JOURNAL MEDLINE PUBMED

REFERENCE AUTHORS

Roest Crolius H., Jaillon O., Dasilva C., Ozouf-Costaz C.,
Fizames C., Fischer C., Wincker P., Brottier P., Quetier F.,
Saurin W., Bernot A. and Weissenbach J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

JOURNAL MEDLINE PUBMED

REFERENCE AUTHORS

Genome Res. 10 (7), 939-949 (2000)
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10899143
10835645
Roest Crolius H., Jaillon O., Dasilva C., Ozouf-Costaz C.,
Fizames C., Fischer C., Wincker P., Brottier P., Quetier F.,
Saurin W., Bernot A. and Weissenbach J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

REFERENCE AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

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REFERENCE 3 (bases 1 to 60)
AUTHORS   Genoscope.
TITLE     Direct Submission
JOURNAL   Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT   This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
    source
        Location/Qualifiers
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                /organism="Tetraodon nigroviridis"
                /mol_type="genomic DNA"
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ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RC 4
      ||
      12 RC 11

RESULT 135
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LOCUS       AY431565               61 bp     mRNA     linear     HTC 24-JUN-2004
DEFINITION   Aedes aegypti ASAP ID: 38007 unknown mRNA sequence.
ACCESSION   AY431565
VERSION     AY431565.1   GI:42763707
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1 (bases 1 to 61)
AUTHORS     Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J.,
            Tsai,S.-P., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
TITLE       Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
JOURNAL     Infect. Immun. 72 (7), 4114-4126 (2004)
PUBMED     15213157
REFERENCE   2 (bases 1 to 61)
AUTHORS     Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.F., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-P., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
TITLE       Direct Submission
JOURNAL     Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES
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                hours post-inoculation"
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                        bacteria-inoculated organisms at 1, 3, 6, 12, and 24
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hours post-inoculation"
/db_xref="taxon:7159"
/sex="female"
/cell_type="hemocyte"
/tissue_type="hemolymph"
/dev_stage="adult"
/note="ASAP-UW Feature ID: 38006"
1..61
/note="unknown; ASAP-UW Feature ID: 38007"
ORIGIN
Query Match      20.0%; Score 2; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GY 8
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      26 GY 27

RESULT 136
AY431565/c
LOCUS       AY431565               61 bp     mRNA     linear     HTC 24-JUN-2004
DEFINITION   Aedes aegypti ASAP ID: 38007 unknown mRNA sequence.
ACCESSION   AY431565
VERSION     AY431565.1   GI:42763707
KEYWORDS    HTC.
SOURCE      Aedes aegypti (yellow fever mosquito)
ORGANISM    Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1 (bases 1 to 61)
AUTHORS     Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Fuchs,J.F., Liss,P., Rusch,M., Butler,K.M., Wu,R.C.-C., Lin,S.-P.,
            Kuo,H.-Y., Tsao,I.-Y., Huang,C.-Y., Liu,T.-T., Hsiao,K.-J.,
            Tsai,S.-F., Yang,U.-C., Nappi,A.J., Perna,N.T., Chen,C.-C. and
            Christensen,B.M.
TITLE       Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
JOURNAL     Infect. Immun. 72 (7), 4114-4126 (2004)
PUBMED     15213157
REFERENCE   2 (bases 1 to 61)
AUTHORS     Bartholomay,L.C., Cho,W.-L., Rocheleau,T.A., Boyle,J.P., Beck,E.T.,
            Liss,P., Rusch,M., Fuchs,J.P., Butler,K.M., Wu,R.C.-C., Kuo,H.-K.,
            Tsao,I.-Y., Huang,C.-Y., Hsiao,K.-J., Tsai,S.-F., Yang,U.-C.,
            Nappi,A.J., Perna,N.T., Chen,C.-C. and Christensen,B.M.
TITLE       Direct Submission
JOURNAL     Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT     More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES
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            1..61
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                /mol_type="mRNA"
                /strain="liverpool"
                /isolation_source="perfused hemolymph of
                bacteria-inoculated organisms at 1, 3, 6, 12, and 24
                hours post-inoculation"
                /db_xref="taxon:7159"
                /sex="female"
                /cell_type="hemocyte"
                /tissue_type="hemolymph"
                /dev_stage="adult"
                /note="ASAP-UW Feature ID: 38006"
            1..61
                /note="unknown; ASAP-UW Feature ID: 38007"
            misc_feature
                Location/Qualifiers
                    1..61
                        /organism="Aedes aegypti"
                        /mol_type="mRNA"
                        /strain="liverpool"
                        /isolation_source="perfused hemolymph of
                        bacteria-inoculated organisms at 1, 3, 6, 12, and 24
                        hours post-inoculation"
                        /db_xref="taxon:7159"
                        /sex="female"
                        /cell_type="hemocyte"
                        /tissue_type="hemolymph"
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                    1..61
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            ORIGIN

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Query Match      20.0%; Score 2; DB 3; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RC 4
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Db      27 RC 26

RESULT 137
AY432562
LOCUS      AY432562
DEFINITION Aedes aegypti 61 bp mRNA linear HTC 24-JUN-2004
ACCESSION AY432562
VERSION    AY432562.1 GI:42763799
KEYWORDS   HTC
SOURCE     Aedes aegypti (yellow fever mosquito)
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1 (bases 1 to 61)
AUTHORS    Bartholomay L.C., Cho W.-L., Rocheleau T.A., Boyle J.P., Beck E.T.,
            Fuchs J.F., Liss P., Ruch M., Butler K.M., Wu R.C.-C., Lin S.-P.,
            Kuo H.-Y., Tsao I.-Y., Huang C.-Y., Liu T.-T., Hsiao K.-J.,
            Tsai S.-F., Yang U.-C., Nappi A.J., Perna N.T., Chen C.-C. and
            Christensen B.M.
TITLE      Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
JOURNAL    Infect. Immun. 72 (7), 4114-4126 (2004)
PUBMED     15213157
REFERENCE   2 (bases 1 to 61)
AUTHORS    Bartholomay L.C., Cho W.-L., Rocheleau T.A., Boyle J.P., Beck E.T.,
            Liss P., Ruch M., Fuchs J.F., Butler K.M., Wu R.C.-C., Lin S.-P.,
            Tsao I.-Y., Huang C.-Y., Hsiao K.-J., Tsai S.-F., Yang U.-C.,
            Nappi A.J., Perna N.T., Chen C.-C. and Christensen B.M.
TITLE      Direct Submission
JOURNAL    Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT    More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES   Location/Qualifiers
            source
              1..61
                /organism="Aedes aegypti"
                /mol_type="mRNA"
                /strain="liverpool"
                /isolation_source="perfused hemolymph of
                bacteria-inoculated organisms at 1, 3, 6, 12, and 24
                hours post-inoculation"
                /db_xref="taxon:7159"
                /sex="female"
                /cell_type="hemocyte"
                /tissue_type="hemolymph"
                /dev_stage="adult"
                /note="ASAP-UW Feature ID: 37032"
            misc_feature
              1..61
                /note="unknown; ASAP-UW Feature ID: 37033"
            ORIGIN
            Query Match      20.0%; Score 2; DB 3; Length 61;
            Best Local Similarity 100.0%; Pred. No. 0;
            Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RC 4
      ||
Db      27 RC 28

RESULT 139
AY432871
LOCUS      AY432871
DEFINITION Aedes aegypti 61 bp mRNA linear HTC 24-JUN-2004
ACCESSION AY432871
VERSION    AY432871.1 GI:42763173
KEYWORDS   HTC
SOURCE     Aedes aegypti (yellow fever mosquito)
ORGANISM   Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
            Stegomyia.
REFERENCE   1 (bases 1 to 61)
AUTHORS    Bartholomay L.C., Cho W.-L., Rocheleau T.A., Boyle J.P., Beck E.T.,
            Fuchs J.F., Liss P., Ruch M., Butler K.M., Wu R.C.-C., Lin S.-P.,
            Kuo H.-Y., Tsao I.-Y., Huang C.-Y., Liu T.-T., Hsiao K.-J.,
            Tsai S.-F., Yang U.-C., Nappi A.J., Perna N.T., Chen C.-C. and
            Christensen B.M.
TITLE      Description of the Transcriptomes of Immune Response-Activated
            Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
            subalbatus
JOURNAL    Infect. Immun. 72 (7), 4114-4126 (2004)
PUBMED     15213157
REFERENCE   2 (bases 1 to 61)
AUTHORS    Bartholomay L.C., Cho W.-L., Rocheleau T.A., Boyle J.P., Beck E.T.,
            Liss P., Ruch M., Fuchs J.F., Butler K.M., Wu R.C.-C., Lin S.-P.,
            Tsao I.-Y., Huang C.-Y., Hsiao K.-J., Tsai S.-F., Yang U.-C.,
            Nappi A.J., Perna N.T., Chen C.-C. and Christensen B.M.
TITLE      Direct Submission
JOURNAL    Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
            University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
            53706, USA
COMMENT    More information about this sequence is available in ASAP (A
            Systematic Annotation Package for community analysis of genomes)
            from the University of Wisconsin-Madison at
            https://asap.ahabs.wisc.edu/annotation/php/logon.php.
FEATURES   Location/Qualifiers
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              1..61
                /organism="Aedes aegypti"
                /mol_type="mRNA"
                /strain="liverpool"
                /isolation_source="perfused hemolymph of
                bacteria-inoculated organisms at 1, 3, 6, 12, and 24
                hours post-inoculation"
                /db_xref="taxon:7159"
                /sex="female"
                /cell_type="hemocyte"
                /tissue_type="hemolymph"
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                /note="ASAP-UW Feature ID: 37032"
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            Query Match      20.0%; Score 2; DB 3; Length 61;
            Best Local Similarity 100.0%; Pred. No. 0;
            Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RC 4
      ||
Db      27 RC 28

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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.

REFERENCE
AUTHORS
 1 (bases 1 to 61)
 Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

TITLE
 Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors *Aedes aegypti* and *Armigeres subalbatus*

JOURNAL
PUBMED
REFERENCE
AUTHORS
 Infect. Immun. 72 (7), 4114-4126 (2004)
 15213157
 2 (bases 1 to 61)
 Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Rusch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K., Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

TITLE
 Direct Submission

JOURNAL
 Submitted (08-OCT-2003) Animal Health and Biomedical Sciences, University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI 53706, USA

COMMENT
 More information about this sequence is available in ASAP (A Systematic Annotation Package for community analysis of genomes) from the University of Wisconsin-Madison at <https://asap.ababs.wisc.edu/annotation/php/logon.php>.

FEATURES
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 /organism="Aedes aegypti"
 /mol_type="mRNA"
 /strain="liverpool"
 /isolation_source="perfused hemolymph of bacteria-inoculated organisms at 1, 3, 6, 12, and 24 hours post-inoculation"
 /db_xref="taxon:7159"
 /sex="female"
 /cell_type="hemocyte"
 /tissue_type="hemolymph"
 /dev_stage="adult"
 /note="ASAP-UW Feature ID: 35498"

misc_feature
 1..61
 /note="unknown; ASAP-UW Feature ID: 35499"

ORIGIN

Query Match 20.0%; Score 2; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 8
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Db 17 GY 18

RESULT 140
AY432871/c
LOCUS
 Aedes aegypti 61 bp mRNA linear HTC 24-JUN-2004
DEFINITION
 Aedes aegypti ASAP ID: 35499 unknown mRNA sequence.
ACCESSION
 AY432871
VERSION
 AY432871.1 GI:42763173
KEYWORDS
 HTC.

ORGANISM
 Aedes aegypti (yellow fever mosquito)
 Aedes aegypti
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes; Stegomyia.

REFERENCE
AUTHORS
 1 (bases 1 to 61)
 Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P., Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

TITLE
 Description of the Transcriptomes of Immune Response-Activated Hemocytes from the Mosquito Vectors *Aedes aegypti* and *Armigeres*

JOURNAL
PUBMED
REFERENCE
AUTHORS
 Infect. Immun. 72 (7), 4114-4126 (2004)
 15213157
 2 (bases 1 to 61)
 Bartholomay, L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T., Liss, P., Rusch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K., Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

TITLE
 Direct Submission

JOURNAL
 Submitted (08-OCT-2003) Animal Health and Biomedical Sciences, University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI 53706, USA

COMMENT
 More information about this sequence is available in ASAP (A Systematic Annotation Package for community analysis of genomes) from the University of Wisconsin-Madison at <https://asap.ababs.wisc.edu/annotation/php/logon.php>.

FEATURES
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 Location/Qualifiers
 1..61
 /organism="Aedes aegypti"
 /mol_type="mRNA"
 /strain="liverpool"
 /isolation_source="perfused hemolymph of bacteria-inoculated organisms at 1, 3, 6, 12, and 24 hours post-inoculation"
 /db_xref="taxon:7159"
 /sex="female"
 /cell_type="hemocyte"
 /tissue_type="hemolymph"
 /dev_stage="adult"
 /note="ASAP-UW Feature ID: 35498"

misc_feature
 1..61
 /note="unknown; ASAP-UW Feature ID: 35499"

ORIGIN

Query Match 20.0%; Score 2; DB 3; Length 61;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4
 ||
Db 18 RC 17

RESULT 141
L76124
LOCUS
 L76124 61 bp mRNA linear EST 21-FEB-1996
DEFINITION
 SCMRAP0218 G2/KS adult worm mini-library Schistosoma mansoni cDNA clone SMRAP0218, mRNA sequence.
ACCESSION
 L76124
VERSION
 L76124.1 GI:1196862
KEYWORDS
 EST.

SOURCE
 Schistosoma mansoni
 Schistosoma mansoni
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoida; Schistosomatoidea; Schistosomatidae; Schistosoma.

REFERENCE
AUTHORS
 1 (bases 1 to 61)
 Neto, E.D., Harrop, R., Correa-Oliveira, R., Wilson, R.A., Pena, S.D. and Simpson, A.J.G.

TITLE
 Minilibraries constructed from cDNA generated by arbitrarily primed RT-PCR: an alternative to normalized libraries for the generation of ESTs from nanogram quantities of mRNA

JOURNAL
MEDLINE
PUBMED
COMMENT
 Gene 186 (1), 135-142 (1997)
 97199380
 9047356
 Contact: Neto, E.D., Harrop, R., Correa-Oliveira, R., Wilson, R.A., Pena, S.D. and Simpson, A.J.G.

FEATURES
 source
 Location/Qualifiers
 1..61
 /organism="Schistosoma mansoni"
 /mol_type="mRNA"
 /db_xref="taxon:6183"
 /clone="SMRAP0218"
 /clone_lib="G2/KS adult worm mini-library"

/note="A mini-library was made by cloning products derived from RNA-arbitrarily primed PCR (RAP PCR) profiles into the pUC 18 vector. Reverse transcription of adult worm mRNA was primed with G2and subsequent PCR amplification was performed in the presence of primer KS"

ORIGIN

Query Match 20.0%; Score 2; DB 7; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 7 GY 8
Db 34 GY 35

RESULT 142
L76124/c

LOCUS L76124 61 bp mRNA linear EST 21-FEB-1996
DEFINITION SCMRAP0218 G2/KS adult worm mini-library Schistosoma mansoni CDNA
clone SMRAP0218, mRNA sequence.

ACCESSION L76124
VERSION L76124.1 GI:1196862

KEYWORDS EST.

SOURCE Schistosoma mansoni

ORGANISM Schistosoma mansoni

REFERENCE 1 (bases 1 to 61)
AUTHORS Rukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigoidida; Schistosomatidae; Schistosomatidae; Schistosoma.

TITLE Neto,E.D., Harrop,R., Correa-Oliveira,R., Wilson,R.A., Pena,S.D. and Simpson,A.J.G.

Manilibraries constructed from cDNA generated by arbitrarily primed RT-PCR: an alternative to normalized libraries for the generation of ESTs from nanogram quantities of mRNA
Gene 186 (1), 135-142 (1997)

JOURNAL 97199380

MEDLINE 9047356

PUBMED

COMMENT Contact: Neto,E.D., Harrop,R., Correa-Oliveira,R., Wilson,R.A., Pena,S.D. and Simpson,A.J.

FEATURES
source

1. .61
Location/Qualifiers
/organism="Schistosoma mansoni"
/mol_type="mRNA"
/db_xref="taxon:6183"
/clone_lib="SMRAP0218"

/note="A mini-library was made by cloning products derived from RNA-arbitrarily primed PCR (RAP PCR) profiles into the pUC 18 vector. Reverse transcription of adult worm mRNA was primed with G2and subsequent PCR amplification was performed in the presence of primer KS"

ORIGIN

Query Match 20.0%; Score 2; DB 7; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 RC 4
Db 44 RC 43

RESULT 143

CNS0139J

LOCUS

DEFINITION CNS0139J 61 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN09E06 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

ACCESSION AL102577

VERSION AL102577.1 GI:5614188

KEYWORDS GSS.

SOURCE Drosophila melanogaster (fruit fly)

ORGANISM Drosophila melanogaster

REFERENCE
AUTHORS

TITLE

JOURNAL

COMMENT

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1. (bases 1 to 61)
Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.

FEATURES

source

1. .61
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN09E06"
/clone_lib="DrosBAC"
/plasmid="pBelOBAC11"
/note="end : T7"

ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 WG 7
Db 47 WG 48

RESULT 144

CNS0139J/c

LOCUS

DEFINITION

CNS0139J 61 bp DNA linear GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN09E06 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

AL102577

AL102577.1 GI:5614188

GSS.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1. (bases 1 to 61)
Genoscope.

Direct Submission

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelOBAC11.

FEATURES

source

1. .61
Location/Qualifiers
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN09E06"
/clone_lib="DrosBAC"
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/note="end : T7"

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ORIGIN
Query Match          20.0%; Score 2; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 5
   ||
Db 48 CW 47

RESULT 145
CNS02J97
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
143G23 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION
AL199924
VERSION
AL199924.1 GI:7838075
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.

REFERENCE
1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL
Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE
20296633
PUBMED
10835645
REFERENCE
2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL
Genome Res. 10 (7), 939-949 (2000)
MEDLINE
20359837
PUBMED
10899143
REFERENCE
3 (bases 1 to 61)
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
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/mol_type="genomic DNA"
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/clone_lib="G"
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PUC-Ori"

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CW 5
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Db 23 CW 22

RESULT 147
CNS02MP4
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
149J04 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION
AL204385
VERSION
AL204385.1 GI:7863204

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KEYWORDS
SOURCE      GSS; genome survey sequence.
ORGANISM    Tetraodon nigroviridis

REFERENCE
AUTHORS     Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
            Estimate of human gene number provided by genome-wide analysis
            using Tetraodon nigroviridis DNA sequence
            Nat. Genet. 25 (2), 235-238 (2000)
            20296633
            PUBMED
            10835645
            REFERENCE
            2

TITLE
JOURNAL     Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
MEDLINE     Fizames,C., Fischer,C., Wincker,P., Brottier,P., Quetier,F.,
PUBMED      Saurin,W., Bernot,A. and Weissenbach,J.
            Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
            Genome Res. 10 (7), 939-949 (2000)
            20359837
            PUBMED
            10899143
            REFERENCE
            3 (bases 1 to 61)
            Genoscope.
            2
            Direct Submission
            Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
1..61
/organism="Tetraodon nigroviridis"
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WG 7
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Db      22 WG 21

RESULT 149
LOCUS    CNS03955
DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
          006P23 of library G from Tetraodon nigroviridis, genomic survey
          sequence.
ACCESSION AL233474.1
VERSION   AL233474.1 GI:7892609
KEYWORDS  GSS; genome survey sequence.
SOURCE    Tetraodon nigroviridis
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
          Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
          Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS   Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
          Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
          Saurin,W. and Weissenbach,J.
          Estimate of human gene number provided by genome-wide analysis
          using Tetraodon nigroviridis DNA sequence
          Nat. Genet. 25 (2), 235-238 (2000)
          20296633
          PUBMED
          10835645
          REFERENCE
          2

TITLE
JOURNAL     Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
MEDLINE     Fizames,C., Fischer,C., Wincker,P., Brottier,P., Quetier,F.,
PUBMED      Saurin,W., Bernot,A. and Weissenbach,J.
            Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
            Genome Res. 10 (7), 939-949 (2000)
            20359837
            PUBMED
            10899143
            REFERENCE
            3 (bases 1 to 61)
            Genoscope.
            2
            Direct Submission
            Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
            BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
            - Web : www.genoscope.cns.fr)
            This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
1..61
/organism="Tetraodon nigroviridis"
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/clone_lib="G"
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CW 5
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Db      21 CW 22

RESULT 148
CNS02MP4/c
LOCUS    CNS02MP4/c
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
          149J04 of library G from Tetraodon nigroviridis, genomic survey
          sequence.
ACCESSION AL204385
VERSION   AL204385.1 GI:7863204
KEYWORDS  GSS; genome survey sequence.
SOURCE    Tetraodon nigroviridis
ORGANISM  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
          Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
          Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE 1
AUTHORS   Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
          Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
          Saurin,W. and Weissenbach,J.

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JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3 (bases 1 to 61)
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source

1. .61
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RC 4

Db 56 RC 57

RESULT 150

CNS03955/c

LOCUS

Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
006P23 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION

AL233474

VERSION

AL233474.1 GI:7892609

KEYWORDS

GSS; genome survey sequence.

SOURCE

Tetraodon nigroviridis

ORGANISM

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

1

Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.

Saurin,W. and Weissenbach,J.

Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

20296633

PUBMED

10835645

REFERENCE

2

Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.

Saurin,W., Bernot,A. and Weissenbach,J.

Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837

PUBMED

10899143

REFERENCE

3 (bases 1 to 61)

Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large

scale clone-end sequencing project of the Tetraodon nigroviridis

genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source

1. .61
Location/Qualifiers
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
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/note="Genoscope sequence ID : COBG006CH12SP1-end :
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Query Match 20.0%; Score 2; DB 9; Length 61;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 8

Db 57 GY 56

RESULT 151

CNS03UDP

LOCUS

Tetraodon nigroviridis genome survey sequence T7 and of clone
058P02 of library G from Tetraodon nigroviridis, genomic survey
sequence.

ACCESSION

AL260998

VERSION

AL260998.1 GI:7982623

KEYWORDS

GSS; genome survey sequence.

SOURCE

Tetraodon nigroviridis

ORGANISM

Tetraodon nigroviridis

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

1

Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.

Saurin,W. and Weissenbach,J.

Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

20296633

PUBMED

10835645

REFERENCE

2

Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.

Saurin,W., Bernot,A. and Weissenbach,J.

Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837

PUBMED

10899143

REFERENCE

3 (bases 1 to 61)

Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES

source

1. .61

Location/Qualifiers

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/clone_lib="G"

/note="Genoscope sequence ID : COBG058DC01LP1-end : T7"

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QY 3 RC 4
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Db 3 RC 4

RESULT 152
CNS044FV/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
058F02 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL260398
AL260398.1 GI:7982623
GSS; genome survey sequence.
Tetraodon nigroviridis
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
2
REFERENCE
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
3 (bases 1 to 61)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
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/db_xref="taxon:99883"
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CY 8
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Db 4 CY 3

RESULT 154
CNS044FV/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
081B01 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL274036
AL274036.1 GI:7996303
GSS; genome survey sequence.
1
REFERENCE
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
2
REFERENCE
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
3 (bases 1 to 61)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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PUC-Ori"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CY 8
   ||
Db 36 CY 37

RESULT 154
CNS044FV/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
081B01 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL274036
AL274036.1 GI:7996303
GSS; genome survey sequence.
1
REFERENCE
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
2
REFERENCE
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
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Nat. Genet. 25 (2), 235-238 (2000)
20296633
10835645
3 (bases 1 to 61)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
Location/Qualifiers
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PUC-Ori"

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SOURCE
ORGANISM Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Perciformes; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
1
REFERENCE
AUTHORS Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
TITLE Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
REFERENCE
AUTHORS 2
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE
AUTHORS 3 (bases 1 to 61)
Genoscope.
Direct Submission
TITLE Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
source Location/Qualifiers
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PUC-Ori"
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 RC 4
||
Db 37 RC 36

RESULT 155
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LOCUS AW059587 62 bp mRNA linear EST 23-AUG-2000
DEFINITION HUTH.bsst.dnc15.final.cluster.77 (3) DNC15 Homo sapiens cDNA
similar to ribosomal protein L23A, mRNA sequence.
ACCESSION AW059587
VERSION AW059587.1 GI:6651909
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 62)
Brenner,S., Williams,S.R., Vermaas,E.H., Storck,T., Moon,K.,
McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
Burcham,T. and Albrecht,G.
In vitro cloning of complex mixtures of DNA on microbeads: Physical
separation of differentially expressed cDNAs
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
20144098
10677516
COMMENT Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338
Fax: 510 670 9302
Email: timb@lynxgen.com
Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the down-regulated gate. Consensus sequence of 3
sequences in cluster.
High quality sequence stop: 62.
FEATURES
source Location/Qualifiers
1. .62
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cells non-induced (treated with DMSO only)."
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Query Match 20.0%; Score 2; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 3 RC 4
||
Db 21 RC 22

RESULT 156
AW059587/c
LOCUS AW059587 62 bp mRNA linear EST 23-AUG-2000
DEFINITION HUTH.bsst.dnc15.final.cluster.77 (3) DNC15 Homo sapiens cDNA
similar to ribosomal protein L23A, mRNA sequence.
ACCESSION AW059587
VERSION AW059587.1 GI:6651909
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 62)
Brenner,S., Williams,S.R., Vermaas,E.H., Storck,T., Moon,K.,
McCollum,C., Mao,J.I., Kirchner,J.J., Eletr,S., DuBridge,R.B.,
Burcham,T. and Albrecht,G.
In vitro cloning of complex mixtures of DNA on microbeads: Physical
separation of differentially expressed cDNAs
Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)
20144098
10677516
COMMENT Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338
Fax: 510 670 9302
Email: timb@lynxgen.com
Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the down-regulated gate. Consensus sequence of 3
sequences in cluster.
High quality sequence stop: 62.
FEATURES
source Location/Qualifiers
1. .62
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="monocytic leukemia"
/cell_line="THP-1 (TIB-202)"
/clone_lib="DNC15"

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/note="Vector: pCR2.1; Cloning of PCR products from micro-beads carrying 3', end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."

ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 WG 7
Db 61 WG 60

RESULT 157

AW059628
LOCUS HUTH.best.dnc15.final.cluster_118_2) DNC15 Homo sapiens cDNA, mRNA
DEFINITION sequence.

ACCESSION

AW059628

KEYWORDS

EST.

SOURCE

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Brenner, S., Williams, S.R., Vermaas, E.H., Storck, T., Moon, K.,
McCollum, C., Mao, J.I., Kirchner, J.J., Eletr, S., DuBridge, R.B.,
Burcham, T. and Albrecht, G.

TITLE

In vitro cloning of complex mixtures of DNA on microbeads: Physical separation of differentially expressed cDNAs

JOURNAL

Proc. Natl. Acad. Sci. U.S.A. 97 (4), 1665-1670 (2000)

MEDLINE

PUBMED

COMMENT

10677516
Contact: Burcham TS
LYNX Therapeutics, Inc.
25861 Industrial Blvd., Hayward, CA 94545, USA
Tel: 510 670 9338
Fax: 510 670 9302
Email: timb@lynxgen.com
Sequence obtained from LYNX Therapeutics Megasort technology.
Collected from the down-regulated gate. Consensus sequence of 2
sequences in cluster.
High quality sequence stop: 62.
Location/Qualifiers

FEATURES

source

1..62
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="monocytic leukemia"
/cell_line="THP-1 (TIB-202)"
/clone_lib="DNC15"
/note="Vector: pCR2.1; Cloning of PCR products from micro-beads carrying 3', end of down-regulated cDNA. THP-1 cells non-induced (treated with DMSO only)."

ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 7 GY 8
Db 61 GY 62

RESULT 158

AW059628/c
LOCUS HUTH.best.dnc15.final.cluster_118_2) DNC15 Homo sapiens cDNA, mRNA
DEFINITION sequence.

ACCESSION

AW059628

VERSION

AW059628.1 GI:6651950

KEYWORDS

SOURCE

ORGANISM

Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 62)
Brenner, S., Williams, S.R., Vermaas, E.H., Storck, T., Moon, K.,
McCollum, C., Mao, J.I., Kirchner, J.J., Eletr, S., DuBridge, R.B.,
Burcham, T. and Albrecht, G.

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

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FEATURES
  source
    Location/Qualifiers
      1. .62
        /organism="Columba livia"
        /mol_type="mRNA"
        /db_xref="taxon:9932"
        /tissue_type="brain"
        /dev_stage="adult"
        /clone_lib="Pigeon optic tecta cDNA library generated with
        SSH methodology"
        /note="vector: pBluescript(sk-); It was prepared with
        suppression subtractive hybridization (SSH).
        TAG_ISSUE=Brain (optic tecta)
        TAG_SEQ=Not found"

ORIGIN
  Query Match      20.0%; Score 2; DB 2; Length 62;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WW 6
   ||
Db 18 WW 19

RESULT 160
BE577741/c
LOCUS
DEFINITION EST011 Pigeon optic tecta cDNA library generated with SSH
methodology Columba livia CDNA 5', mRNA sequence.
ACCESSION BE577741
VERSION BE577741.1 GI:9828687
KEYWORDS EST.
SOURCE Columba livia (domestic pigeon)
ORGANISM Columba livia
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Archosauria; Aves; Neognathae; Columbiformes; Columba.
TITLE Wang, Y., Xu, L. and Qi, M.
Differentially expressed genes in the pigeon optic tecta after
monocular deprivation
JOURNAL Unpublished (2001)
COMMENT Contact: Wang, Y.
Molecular Biology
Tongji University School of Medicine
1238 Gonghexin Road, Shanghai, 200070, P. R. China
Tel: 021 6634 4540
Email: ywange@public2.sta.net.cn
Seq primer: T7
High quality sequence stop: 62
POLYA=No.

FEATURES
  source
    Location/Qualifiers
      1. .62
        /organism="Columba livia"
        /mol_type="mRNA"
        /db_xref="taxon:9932"
        /tissue_type="brain"
        /dev_stage="adult"
        /clone_lib="Pigeon optic tecta cDNA library generated with
        SSH methodology"
        /note="vector: pbluescript(sk-); It was prepared with
        suppression subtractive hybridization (SSH).
        TAG_ISSUE=Brain (optic tecta)
        TAG_SEQ=Not found"

ORIGIN
  Query Match      20.0%; Score 2; DB 2; Length 62;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WW 6
   ||
Db 19 WW 18

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```

RESULT 161
AY433080
LOCUS
DEFINITION Aedes aegypti ASAP ID: 37497 unknown mRNA sequence.
ACCESSION AY433080
VERSION AY433080.1 GI:42761952
KEYWORDS HTC.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Aedes;
Stegomyia.
REFERENCE 1 (bases 1 to 62)
AUTHORS Bartholomay, L.C., Cho, W.-L., Rochelleau, T.A., Boyle, J.P., Beck, E.T.,
Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P.,
Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J.,
Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and
Christensen, B.M.
Description of the Transcriptomes of Immune Response-Activated
Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres
subalbatus
JOURNAL Infect. Immun. 72 (7), 4114-4126 (2004)
PUBMED 15213157
REFERENCE 2 (bases 1 to 62)
AUTHORS Bartholomay, L.C., Cho, W.-L., Rochelleau, T.A., Boyle, J.P., Beck, E.T.,
Liss, P., Rusch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K.,
Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C.,
Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.
Direct Submission
Submitted (08-OCT-2003) Animal Health and Biomedical Sciences,
University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
53706, USA
More information about this sequence is available in ASAP (A
Systematic Annotation Package for community analysis of genomes)
from the University of Wisconsin-Madison at
https://asap.ahabs.wisc.edu/annotation/php/logon.php.

FEATURES
  source
    Location/Qualifiers
      1. .62
        /organism="Aedes aegypti"
        /mol_type="mRNA"
        /strain="liverpool"
        /isolation_source="perfused hemolymph of
        bacteria-inoculated organisms at 1, 3, 6, 12, and 24
        hours post-innoculation"
        /db_xref="taxon:7159"
        /sex="female"
        /cell_type="hemocyte"
        /tissue_type="hemolymph"
        /dev_stage="adult"
        /note="ASAP-UW Feature ID: 37496"

misc_feature 1. .62
  /note="unknown; ASAP-UW Feature ID: 37497"

ORIGIN
  Query Match      20.0%; Score 2; DB 3; Length 62;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
   ||
Db 14 CW 15

RESULT 162
AY433080/c
LOCUS
DEFINITION Aedes aegypti ASAP ID: 37497 unknown mRNA sequence.
ACCESSION AY433080
VERSION AY433080.1 GI:42761952
KEYWORDS HTC.
SOURCE Aedes aegypti (yellow fever mosquito)
ORGANISM Aedes aegypti

```



```

/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR36E10"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 62;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CW 5
      ||
Db      49 CW 50

RESULT 170
CNS001G1/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence TET3 end of BAC;
BACR36E10 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION
AL074751.1 GI:4954531
VERSION
GSS.
KEYWORDS
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 62)
AUTHORS
Genoscope.
TITLES
Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL
Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES
Location/Qualifiers
1..62
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACR36E10"
/clone_lib="RPCI-98"
/note="end : TET3"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 62;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 WG 7
      ||
Db      50 WG 49

RESULT 171
CNS0119R
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC BACN05E01 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION
AL099993.1 GI:5611604
VERSION
GSS.
KEYWORDS
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 62)
AUTHORS
Genoscope.
TITLES
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CRPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.
FEATURES
Location/Qualifiers
1..62
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN05E01"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : T7"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 62;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GY 8
      ||
Db      22 GY 23

RESULT 172
CNS0119R/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC BACN05E01 of DrosBAC library from Drosophila melanogaster (fruit fly), genomic survey sequence.
ACCESSION
AL099993.1 GI:5611604
VERSION
GSS.
KEYWORDS
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 62)
AUTHORS
Genoscope.
TITLES
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
JOURNAL
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CRPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBelobAC11.
FEATURES
Location/Qualifiers
1..62
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN05E01"
/clone_lib="DrosBAC"
/plasmid="pBelobAC11"
/note="end : T7"

ORIGIN
Query Match      20.0%; Score 2; DB 9; Length 62;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GY 8
      ||
Db      22 GY 23

```

FEATURES
source

Location/Qualifiers
1. .62
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
/db_xref="taxon:7227"
/clone="BACN05E01"
/clone_lib="DrosBAC"
/plasmid="pBelOBAC11"
/note="end : T7"

ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 62;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RC 4
DB 23 RC 22

RESULT 173

CNS02QCA

LOCUS

DEFINITION Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 157D21 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION

AL209107

AL209107.1 GI:7867926

GSS; genome survey sequence.

KEYWORDS

SOURCE

ORGANISM

Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

AUTHORS

Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W., and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

20296633

PUBMED

10835645

REFERENCE

AUTHORS

Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A., and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837

PUBMED

10899143

REFERENCE

AUTHORS

3 (bases 1 to 62)

Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

FEATURES

source

1. .62
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="157D21"
/clone_lib="G"
/note="Genoscope sequence ID : COAGI57CB11SP1-end :
PUC-Ori"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 2; DB 9; Length 62;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

4 CW 5

DB

55 CW 56

RESULT 174

CNS02QCA/c

LOCUS

DEFINITION

Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone 157D21 of library G from Tetraodon nigroviridis, genomic survey sequence.

ACCESSION

AL209107

AL209107.1 GI:7867926

GSS; genome survey sequence.

KEYWORDS

SOURCE

ORGANISM

Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE

AUTHORS

Roest Crollius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
Saurin, W., and Weissenbach, J.

Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence

Nat. Genet. 25 (2), 235-238 (2000)

20296633

PUBMED

10835645

REFERENCE

AUTHORS

Roest Crollius, H., Jaillon, O., Dasilva, C., Ozouf-Costaz, C.,
Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A., and Weissenbach, J.

Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis

Genome Res. 10 (7), 939-949 (2000)

20359837

PUBMED

10899143

REFERENCE

AUTHORS

3 (bases 1 to 62)

Genoscope.

Direct Submission

Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at

http://www.genoscope.cns.fr/Tetraodon.

Location/Qualifiers

FEATURES

source

1. .62
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="157D21"
/clone_lib="G"
/note="Genoscope sequence ID : COAGI57CB11SP1-end :
PUC-Ori"

ORIGIN

Query Match

Best Local Similarity 100.0%; Score 2; DB 9; Length 62;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

6 WG 7

DB

56 WG 55

Mushroom Research Laboratory, Department of Plant Pathology
The Pennsylvania State University
305 Buckhout, University Park, PA 16802, USA
Tel: 8148633073
Fax: 8148637217
Email: mxoll@psu.edu
Seq primer: T7.

FEATURES

source
1. .63
Location/Qualifiers
/organism="Agaricus bisporus"
/mol_type="mRNA"
/strain="Sylvan-130"
/db_xref="taxon:5341"
/tissue_type="Basidiome"
/clone_lib="Basidiome cDNA library"
/note="Vector: pBluescript II SK (+); Site_1: SalI;
Site_2: NotI"

ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RC 4
||
Db 28 RC 29

RESULT 178

AW444235/c
LOCUS
DEFINITION
AB555 Basidiome cDNA library Agaricus bisporus cDNA 5', mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Agaricus bisporus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Agaricaceae; Agaricus.

REFERENCE
AUTHORS
TITLE
Ospina-Giraldo, M.D., Collopy, P.D., Romaine, C.P. and Royse, D.J.
Classification of sequences expressed during the primordial and
basidiome stages of the cultivated mushroom Agaricus bisporus
Fungal Genet. Biol. 29 (2), 81-94 (2000)

JOURNAL

MEDLINE
PUBMED

20374017
10919377
Contact: Manuel D. Ospina-Giraldo
Mushroom Research Laboratory, Department of Plant Pathology
The Pennsylvania State University
305 Buckhout, University Park, PA 16802, USA
Tel: 8148633073
Fax: 8148637217
Email: mxoll@psu.edu
Seq primer: T7.

FEATURES

source
1. .63
Location/Qualifiers
/organism="Agaricus bisporus"
/mol_type="mRNA"
/strain="Sylvan-130"
/db_xref="taxon:5341"
/tissue_type="Basidiome"
/clone_lib="Basidiome cDNA library"
/note="Vector: pBluescript II SK (+); Site_1: SalI;
Site_2: NotI"

ORIGIN

Query Match 20.0%; Score 2; DB 2; Length 63;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 8
||

Db 29 GY 28

RESULT 179

AW444251
LOCUS
DEFINITION
AB015 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Agaricus bisporus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Agaricaceae; Agaricus.

REFERENCE
AUTHORS
TITLE
Ospina-Giraldo, M.D., Collopy, P.D., Romaine, C.P. and Royse, D.J.
Classification of sequences expressed during the primordial and
basidiome stages of the cultivated mushroom Agaricus bisporus
Fungal Genet. Biol. 29 (2), 81-94 (2000)

JOURNAL

MEDLINE
PUBMED

20374017
10919377
Contact: Manuel D. Ospina-Giraldo
Mushroom Research Laboratory, Department of Plant Pathology
The Pennsylvania State University
305 Buckhout, University Park, PA 16802, USA
Tel: 8148633073
Fax: 8148637217
Email: mxoll@psu.edu
Seq primer: T7.

FEATURES

source
1. .63
Location/Qualifiers
/organism="Agaricus bisporus"
/mol_type="mRNA"
/strain="Sylvan-130"
/db_xref="taxon:5341"
/tissue_type="Primordium"
/clone_lib="Primordium cDNA library"
/note="Vector: pBluescript II SK (+); Site_1: SalI;
Site_2: NotI"

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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
||
Db 41 WG 42

RESULT 180

AW444251/c
LOCUS
DEFINITION
AB015 Primordium cDNA library Agaricus bisporus cDNA 5', mRNA
sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

Agaricus bisporus
Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Agaricaceae; Agaricus.

REFERENCE
AUTHORS
TITLE
Ospina-Giraldo, M.D., Collopy, P.D., Romaine, C.P. and Royse, D.J.
Classification of sequences expressed during the primordial and
basidiome stages of the cultivated mushroom Agaricus bisporus
Fungal Genet. Biol. 29 (2), 81-94 (2000)

JOURNAL

MEDLINE
PUBMED

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10919377
Contact: Manuel D. Ospina-Giraldo
Mushroom Research Laboratory, Department of Plant Pathology
The Pennsylvania State University

305 Buckhout, University Park, PA 16802, USA
 Tel: 8148633073
 Fax: 8148637217
 Email: mxoll@psu.edu
 Seq primer: 17.
 Location/Qualifiers

FEATURES

source
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 /organism="Agaricus bisporus"
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 /db_xref="taxon:5341"
 /tissue_type="Primordium"
 /clone_lib="Primordium cDNA library"
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 Site_2: NotI"

ORIGIN

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 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 42 CW 41

RESULT 181

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 LOCUS Armigeres subalbatus ASAP ID: 39257 unknown mRNA sequence.
 DEFINITION
 ACCESSION AY440539
 VERSION AY440539.1 GI:42765568
 KEYWORDS HTC.

SOURCE

ORGANISM Armigeres subalbatus
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
 Armigeres.
 1 (bases 1 to 63)

REFERENCE

2 (bases 1 to 63)
 Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
 Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P.,
 Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J.,
 Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and
 Christensen, B.M.

TITLE

Description of the Transcriptomes of Immune Response-Activated
 Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres

JOURNAL

subalbatus
 Infect. Immun. 72 (7), 4114-4126 (2004)

PUBMED

15213157

REFERENCE

2 (bases 1 to 63)
 Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
 Liss, P., Rusch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K.,
 Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C.,
 Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

TITLE

Direct Submission
 Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,
 University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
 53706, USA

COMMENT

More information about this sequence is available in ASAP (A
 Systematic Annotation Package for community analysis of genomes)
 from the University of Wisconsin-Madison at
<https://asap.ahabs.wisc.edu/annotation/php/logon.php>.

FEATURES

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 /cell_type="hemocyte"
 /tissue_type="hemolymph"

/dev_stage="adult"
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misc_feature

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 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5

Db 23 CW 24

RESULT 182

AY440539 AY440539 63 bp mRNA linear HTC 24-JUN-2004
 LOCUS Armigeres subalbatus ASAP ID: 39257 unknown mRNA sequence.
 DEFINITION
 ACCESSION AY440539
 VERSION AY440539.1 GI:42765568
 KEYWORDS HTC.

SOURCE

ORGANISM Armigeres subalbatus
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
 Armigeres.
 1 (bases 1 to 63)

REFERENCE

2 (bases 1 to 63)
 Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
 Fuchs, J.F., Liss, P., Rusch, M., Butler, K.M., Wu, R.C.-C., Lin, S.-P.,
 Kuo, H.-Y., Tsao, I.-Y., Huang, C.-Y., Liu, T.-T., Hsiao, K.-J.,
 Tsai, S.-F., Yang, U.-C., Nappi, A.J., Perna, N.T., Chen, C.-C. and
 Christensen, B.M.

TITLE

Description of the Transcriptomes of Immune Response-Activated
 Hemocytes from the Mosquito Vectors Aedes aegypti and Armigeres

JOURNAL

subalbatus
 Infect. Immun. 72 (7), 4114-4126 (2004)

PUBMED

15213157

REFERENCE

2 (bases 1 to 63)
 Bartholomay L.C., Cho, W.-L., Rocheleau, T.A., Boyle, J.P., Beck, E.T.,
 Liss, P., Rusch, M., Fuchs, J.F., Butler, K.M., Wu, R.C.-C., Kuo, H.-K.,
 Tsao, I.-Y., Huang, C.-Y., Hsiao, K.-J., Tsai, S.-F., Yang, U.-C.,
 Nappi, A.J., Perna, N.T., Chen, C.-C. and Christensen, B.M.

TITLE

Direct Submission
 Submitted (17-OCT-2003) Animal Health and Biomedical Sciences,
 University of Wisconsin-Madison, 1656 Linden Dr., Madison, WI
 53706, USA

COMMENT

More information about this sequence is available in ASAP (A
 Systematic Annotation Package for community analysis of genomes)
 from the University of Wisconsin-Madison at
<https://asap.ahabs.wisc.edu/annotation/php/logon.php>.

FEATURES

source
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 /organism="Armigeres subalbatus"
 /mol_type="mRNA"
 /isolation_source="perfused hemolymph of
 bacteria-inoculated organisms at 1, 3, 6, 12, and 24
 hours post-inoculation"
 /db_xref="taxon:124917"
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 /cell_type="hemocyte"
 /tissue_type="hemolymph"
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 /note="ASAP-UW Feature ID: 39256"

misc_feature

ORIGIN

Query Match 20.0%; Score 2; DB 3; Length 63;
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FEATURES
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        /note="end : T7"

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RR 2
   ||
Db 43 RR 44

RESULT 186
CNS017GA/c
LOCUS
DEFINITION
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN17003 of DrosBAC library from Drosophila melanogaster (fruit
fly), genomic survey sequence.
ACCESSION
AL108004
VERSION
AL108004.1 GI:5628308
KEYWORDS
GSS.
SOURCE
Drosophila melanogaster (fruit fly)
ORGANISM
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
1 (bases 1 to 63)
AUTHORS
Genoscope.
DIRECT SUBMISSION
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (HDGP) -
http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaut at CESP (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.

FEATURES
  source
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        /plasmid="pBelobAC11"
        /note="end : T7"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 9
   ||
Db 44 YY 43

RESULT 187
CNS01VCH
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
198G06 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL168938
VERSION
AL168938.1 GI:7806995
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

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sequence.
ACCESSION
AL168938
VERSION
AL168938.1 GI:7806995
KEYWORDS
GSS: genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE
1 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
  Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
  Saurin,W. and Weissenbach,J.
  Estimate of human gene number provided by genome-wide analysis
  using Tetraodon nigroviridis DNA sequence
  Nat. Genet. 25 (2), 235-238 (2000)
20296633
PUBMED
10835645
REFERENCE
2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
  Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
  Saurin,W., Bernot,A. and Weissenbach,J.
  Characterization and repeat analysis of the compact genome of the
  freshwater pufferfish Tetraodon nigroviridis
  Genome Res. 10 (7), 939-949 (2000)
20359837
MEDLINE
1089143
PUBMED
3 (bases 1 to 63)
AUTHORS
Genoscope.
DIRECT SUBMISSION
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/tetraodon.
FEATURES
  source
    Location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
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Db 42 CW 43

RESULT 188
CNS01VCH/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
198G06 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL168938
VERSION
AL168938.1 GI:7806995
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Tetraodon nigroviridis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

```

```

REFERENCE
AUTHORS
1 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
  Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
  Saurin,W. and Weissenbach,J.
  Estimate of human gene number provided by genome-wide analysis
  using Tetraodon nigroviridis DNA sequence
JOURNAL MEDLINE
20296633
PUBMED 10835645
REFERENCE
AUTHORS
2 Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
  Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
  Saurin,W., Bernot,A. and Weissenbach,J.
  Characterization and repeat analysis of the compact genome of the
  freshwater pufferfish Tetraodon nigroviridis
JOURNAL MEDLINE
20359837
PUBMED 10899143
REFERENCE
AUTHORS
3 (bases 1 to 63)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
source
1..63
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
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PUC-Ori"
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Query Match 20.0%; Score 2; DB 9; Length 63;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
||
Db 43 WG 42

RESULT 189
CNS02JW3
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
144G12 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL200748
VERSION
AL200748.1 GI:7859093
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL MEDLINE
20296633
PUBMED 10835645
REFERENCE
2

```

```

AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
20359837
PUBMED 10899143
REFERENCE
3 (bases 1 to 63)
Genoscope.
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.
FEATURES
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
||
Db 34 WG 35

RESULT 190
CNS02JW3/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence T7 end of clone
144G12 of library G from Tetraodon nigroviridis, genomic survey
sequence.
ACCESSION
AL200748
VERSION
AL200748.1 GI:7859093
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontoidea; Tetraodontidae; Tetraodon.
REFERENCE
1
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
JOURNAL MEDLINE
20296633
PUBMED 10835645
REFERENCE
2
AUTHORS
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)
20359837
PUBMED 10899143
REFERENCE
3 (bases 1 to 63)
Genoscope.
Direct Submission

```

JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.
FEATURES Location/Qualifiers
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Query Match 20.0%; Score 2; DB 9; Length 63;
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Qy 4 CW 5
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 Db 35 CW 34

RESULT 191
CNS02PAK
LOCUS CNS02PAK 63 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 155M16 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL207749
VERSION AL207749.1 GI:7866568
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS 1 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
 Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
 Nat. Genet. 25 (2), 235-238 (2000)
 20296633
 10835645
TITLE Estimate of human gene number provided by genome-wide analysis
JOURNAL using Tetraodon nigroviridis DNA sequence
MEDLINE Nat. Genet. 25 (2), 235-238 (2000)
PUBMED 20296633
REFERENCE 20296633
 10835645
AUTHORS 2 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
 Genome Res. 10 (7), 939-949 (2000)
 20359837
 10899143
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE Genome Res. 10 (7), 939-949 (2000)
PUBMED 20359837
 10899143
REFERENCE 20359837
 10899143
AUTHORS 3 (bases 1 to 63)
 Genoscope.
 Direct Submission
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.
FEATURES Location/Qualifiers
 source
 1. .63
 /organism="Tetraodon nigroviridis"
 /mol_type="genomic DNA"
 /db_xref="taxon:99883"
 /clone_lib="155M16"
 /clone_lib="G"
 /note="Genoscope sequence ID : C0AG155BG08LPI-end : T7"

ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 63;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
 ||
 Db 52 WG 53

RESULT 192
CNS02PAK/c
LOCUS CNS02PAK 63 bp DNA linear GSS 01-SEP-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone 155M16 of library G from Tetraodon nigroviridis, genomic survey sequence.
ACCESSION AL207749
VERSION AL207749.1 GI:7866568
KEYWORDS GSS; genome survey sequence.
SOURCE Tetraodon nigroviridis
ORGANISM Tetraodon nigroviridis
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
AUTHORS 1 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F., Saurin,W. and Weissenbach,J.
 Estimate of human gene number provided by genome-wide analysis using Tetraodon nigroviridis DNA sequence
 Nat. Genet. 25 (2), 235-238 (2000)
 20296633
 10835645
TITLE Estimate of human gene number provided by genome-wide analysis
JOURNAL using Tetraodon nigroviridis DNA sequence
MEDLINE Nat. Genet. 25 (2), 235-238 (2000)
PUBMED 20296633
REFERENCE 20296633
 10835645
AUTHORS 2 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C., Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and Weissenbach,J.
 Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
 Genome Res. 10 (7), 939-949 (2000)
 20359837
 10899143
TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE Genome Res. 10 (7), 939-949 (2000)
PUBMED 20359837
 10899143
REFERENCE 20359837
 10899143
AUTHORS 3 (bases 1 to 63)
 Genoscope.
 Direct Submission
 Submitted (12-APR-2000) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefgenoscope.cns.fr - Web : www.genoscope.cns.fr)
 This sequence is a single read and was generated as part of a large scale clone-end sequencing project of the Tetraodon nigroviridis genome. For more information, please take a look at <http://www.genoscope.cns.fr/tetraodon>.
FEATURES Location/Qualifiers
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ORIGIN

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 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5

TITLE
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

20296633
10835645

TITLE
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

20359837
10899143

TITLE
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 5
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Db 43 CW 44

RESULT 196
CNS04DE2/c
LOCUS
DEFINITION
Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
102G10 of library G from Tetraodon nigroviridis, genomic survey
sequence.
AL285635
VERSION
AL285635.1 GI:8024061
KEYWORDS
GSS; genome survey sequence.
SOURCE
Tetraodon nigroviridis
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percormorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetraodon.

REFERENCE
1
Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
Saurin,W. and Weissenbach,J.
Estimate of human gene number provided by genome-wide analysis
using Tetraodon nigroviridis DNA sequence
Nat. Genet. 25 (2), 235-238 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

20296633
10835645

TITLE
Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
Saurin,W., Bernot,A. and Weissenbach,J.
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)

JOURNAL
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20359837
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scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
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Db 43 CW 44

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DEFINITION
F1-6D 22 week old human fetal liver cdna library Homo sapiens cdna
clone F1-6D 5', mRNA sequence.
R28845
VERSION
R28845.1 GI:6514217
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 64)
Choi,S., Yun,J.W., Choi,E.K., Cho,Y.G., Sung,Y.C. and Shin,H.S.
Construction of a gene expression profile of a human fetal liver by
single-pass cdna sequencing
Mamm. Genome 6 (9), 653-657 (1995)

JOURNAL
MEDLINE
PUBMED
COMMENT

96081342
8535075

Contact: Hee-Sup Shin
Developmental Genetics
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San31 Hyeodong Pohang, 790-784 Republic of Korea
Tel: 562-279-2291
Fax: 562-279-2199
Email: shinhs@vision.postech.ac.kr
Seq primer: T3 primer.
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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XhoI; The cdna library made by oligo-dr primed and
directionally cloned between 5'ExoR I-XhoI3' sites."

TITLE
Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetraodon nigroviridis
Genome Res. 10 (7), 939-949 (2000)

JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS

20359837
10899143

TITLE
Direct Submission
Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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scale clone-end sequencing project of the Tetraodon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetraodon.

FEATURES
source
1..63
/organism="Tetraodon nigroviridis"
/mol_type="genomic DNA"
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Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WG 7
||
Db 44 WG 43

RESULT 197
R28845
LOCUS
DEFINITION
F1-6D 22 week old human fetal liver cdna library Homo sapiens cdna
clone F1-6D 5', mRNA sequence.
R28845
VERSION
R28845.1 GI:6514217
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 64)
Choi,S., Yun,J.W., Choi,E.K., Cho,Y.G., Sung,Y.C. and Shin,H.S.
Construction of a gene expression profile of a human fetal liver by
single-pass cdna sequencing
Mamm. Genome 6 (9), 653-657 (1995)

JOURNAL
MEDLINE
PUBMED
COMMENT

96081342
8535075

Contact: Hee-Sup Shin
Developmental Genetics
Pohang Institute of Science & Technology
San31 Hyeodong Pohang, 790-784 Republic of Korea
Tel: 562-279-2291
Fax: 562-279-2199
Email: shinhs@vision.postech.ac.kr
Seq primer: T3 primer.
Location/Qualifiers
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/clone_lib="22 week old human fetal liver cdna library"
/note="vector: pBluescriptII SK(-); Site_1: EcoRI; Site_2:
XhoI; The cdna library made by oligo-dr primed and
directionally cloned between 5'ExoR I-XhoI3' sites."

ORIGIN

Query Match 20.0%; Score 2; DB 7; Length 64;
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QY 4 CW 5
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 1 CW 2

Db

RESULT 198

R28845/c
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 DEFINITION F1-6D 22 week old human fetal liver cDNA library Homo sapiens cDNA
 clone F1-6D 5', mRNA sequence.

ACCESSION R28845
 VERSION R28845.1 GI:6514217
 KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS Choi,S.S., Yun,J.W., Choi,E.K., Cho,Y.G., Sung,Y.C. and Shin,H.S.
 TITLE Construction of a gene expression profile of a human fetal liver by
 single-pass cDNA sequencing
 JOURNAL Mamm. Genome 6 (9), 653-657 (1995)
 MEDLINE 96081342
 PUBMED 8535075

COMMENT

Contact: Hee-Sup Shin
 Developmental Genetics
 Pohang Institute of Science & Technology
 San31, Hyodong Pohang, 790-784 Republic of Korea
 Tel: 562-279-2291
 Fax: 562-279-2199
 Email: shinhsv@vision.postech.ac.kr
 Seq primer: T3 primer.

FEATURES

source
 1..64
 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /note="Vector: pBluescriptII SK(-); site 1: EcoRI; Site_2:
 XhoI; The cDNA library made by oligo-dT primed and
 directionally cloned between 5'ExoR I-XhoI3' sites."

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 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WG 7
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 2 WG 1

Db

RESULT 199

CNS00DAF
 LOCUS R28845 64 bp DNA linear GSS 04-JUN-1999
 DEFINITION Drosophila melanogaster genome survey sequence W7 end of BAC #
 BACR27L06 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.

ACCESSION AL060631

VERSION AL060631.1 GI:4947791

KEYWORDS

SOURCE

ORGANISM

Drosophila melanogaster (fruit fly)
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Sphydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 64)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammose in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,

NY. The library is named RPCI-98 and was constructed by partial

EcoRI digestion of Drosophila DNA provided by the BDGP from the

isogenic strain Y2; cn bw sp, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or

filters for hybridization from the BACPAC Resource Center can be

found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

Location/Qualifiers

1..64

/organism="Drosophila melanogaster"

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Best Local Similarity 100.0%; Pred. No. 0;

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||

57 RC 58

Db

RESULT 200

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

COMMENT

AUTHORS

TITLE

JOURNAL

COMMENT

CNS00DAF 64 bp DNA linear GSS 04-JUN-1999

Drosophila melanogaster genome survey sequence W7 end of BAC #

BACR27L06 of RPCI-98 library from Drosophila melanogaster (fruit

fly), genomic survey sequence.

AL060631

AL060631.1 GI:4947791

GSS.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Sphydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 64)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

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The BDGP is constructing a physical map of the Drosophila

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isogenic strain Y2; cn bw sp, the same strain used for the BDGP's

P1 and EST libraries. A more detailed description of the library

and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

FEATURES

source

Location/Qualifiers

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/organism="Drosophila melanogaster"
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ORIGIN

Query Match 20.0%; Score 2; DB 9; Length 64;
Best Local Similarity 100.0%; Pred.No. 0;
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Qy 7 GY 8

Db 58 GY 57

Search completed: January 14, 2005, 17:52:24
Job time : 2736 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: January 14, 2005, 16:25:29 ; Search time 82 Seconds
(without alignments)
86.682 Million cell updates/sec

Title: US-09-813-824A-3
Perfect score: 10
Sequence: 1 RRRCWGYY 10

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 824507 seqs, 355394441 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1022532

Minimum DB seq length: 0

Maximum DB seq length: 100

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA.*

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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7	10	100.0	10	2	US-08-299-074A-3
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26	7	70.0	7	4	US-09-196-099-15
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27	40.0	27	58	4	40.0	27	US-08-471-994-7	Sequence 7, Appl
27	40.0	27	59	4	40.0	27	US-08-471-994-11	Sequence 11, Appl
27	40.0	27	60	4	40.0	27	US-08-471-994-11	Sequence 11, Appl
27	40.0	27	61	4	40.0	27	US-08-154-364-7	Sequence 7, Appl
27	40.0	27	62	4	40.0	27	US-08-154-364-7	Sequence 7, Appl
27	40.0	27	63	4	40.0	27	US-08-397-335-8	Sequence 8, Appl
27	40.0	27	64	4	40.0	27	US-08-397-335-8	Sequence 8, Appl
27	40.0	27	65	4	40.0	27	US-08-397-335-9	Sequence 9, Appl
27	40.0	27	66	4	40.0	27	US-08-397-335-9	Sequence 9, Appl
6	30.0	6	67	3	30.0	6	US-09-347-343-1	Sequence 1, Appl
6	30.0	6	68	3	30.0	6	US-09-347-343-1	Sequence 1, Appl
6	30.0	6	69	3	30.0	6	US-09-347-343-2	Sequence 2, Appl
6	30.0	6	70	3	30.0	6	US-09-347-343-2	Sequence 2, Appl
6	30.0	6	71	3	30.0	6	US-09-936-552A-4	Sequence 4, Appl
6	30.0	6	72	3	30.0	6	US-09-936-552A-4	Sequence 4, Appl
6	30.0	6	73	3	30.0	6	US-09-263-692A-8	Sequence 8, Appl
6	30.0	6	74	3	30.0	6	US-09-263-692A-8	Sequence 8, Appl
8	30.0	8	75	3	30.0	8	US-08-646-301A-9	Sequence 9, Appl
8	30.0	8	76	3	30.0	8	US-08-646-301A-9	Sequence 9, Appl
8	30.0	8	77	3	30.0	8	US-09-305-839-41	Sequence 41, Appl
8	30.0	8	78	3	30.0	8	US-09-305-839-41	Sequence 41, Appl
8	30.0	8	79	3	30.0	8	US-09-347-343-3	Sequence 3, Appl
8	30.0	8	80	3	30.0	8	US-09-347-343-3	Sequence 3, Appl
8	30.0	8	81	3	30.0	8	US-09-347-343-4	Sequence 4, Appl
8	30.0	8	82	3	30.0	8	US-09-347-343-4	Sequence 4, Appl
8	30.0	8	83	3	30.0	8	US-09-263-692A-7	Sequence 7, Appl
8	30.0	8	84	3	30.0	8	US-09-263-692A-7	Sequence 7, Appl
9	30.0	9	85	3	30.0	9	US-07-882-838E-1	Sequence 1, Appl
9	30.0	9	86	3	30.0	9	US-07-882-838E-1	Sequence 1, Appl
9	30.0	9	87	3	30.0	9	US-08-643-886-11	Sequence 11, Appl
9	30.0	9	88	3	30.0	9	US-08-643-886-11	Sequence 11, Appl
10	30.0	10	89	3	30.0	10	US-08-122-433-34	Sequence 34, Appl
10	30.0	10	90	3	30.0	10	US-08-122-433-34	Sequence 34, Appl
10	30.0	10	91	3	30.0	10	US-08-643-886-1	Sequence 1, Appl
10	30.0	10	92	3	30.0	10	US-08-643-886-1	Sequence 1, Appl
10	30.0	10	93	3	30.0	10	US-08-643-886-12	Sequence 12, Appl
10	30.0	10	94	3	30.0	10	US-08-643-886-12	Sequence 12, Appl
10	30.0	10	95	3	30.0	10	US-08-472-809B-5	Sequence 5, Appl
10	30.0	10	96	3	30.0	10	US-08-472-809B-5	Sequence 5, Appl
10	30.0	10	97	3	30.0	10	US-08-481-658B-23	Sequence 23, Appl
10	30.0	10	98	3	30.0	10	US-08-481-658B-23	Sequence 23, Appl
10	30.0	10	99	3	30.0	10	US-08-477-504A-23	Sequence 23, Appl
10	30.0	10	100	3	30.0	10	US-08-477-504A-23	Sequence 23, Appl

c 101	3	30.0	10	2	US-08-486-756A-23	Sequence 23, Appl	c 174	3	30.0	14	4	US-09-318-138-22	Sequence 22, Appl
c 102	3	30.0	10	2	US-08-486-756A-23	Sequence 23, Appl	c 175	3	30.0	14	4	US-09-525-160B-10	Sequence 10, Appl
c 103	3	30.0	10	2	US-08-486-756A-23	Sequence 23, Appl	c 176	3	30.0	14	4	US-09-525-160B-10	Sequence 10, Appl
c 104	3	30.0	10	2	US-08-485-862B-23	Sequence 23, Appl	c 177	3	30.0	14	5	PCT-US94-06456-4	Sequence 4, Appl
c 105	3	30.0	10	3	US-08-787-739-23	Sequence 23, Appl	c 178	3	30.0	14	5	PCT-US94-06456-4	Sequence 4, Appl
c 106	3	30.0	10	3	US-08-787-739-23	Sequence 23, Appl	c 179	3	30.0	14	5	PCT-US94-06456-4	Sequence 4, Appl
c 107	3	30.0	10	3	US-08-742-877-13	Sequence 13, Appl	c 180	3	30.0	14	5	PCT-US94-06456-4	Sequence 33, Appl
c 108	3	30.0	10	3	US-08-742-877-13	Sequence 13, Appl	c 181	3	30.0	15	1	US-08-643-886-5	Sequence 5, Appl
c 109	3	30.0	10	3	US-08-487-077A-23	Sequence 23, Appl	c 182	3	30.0	15	1	US-08-643-886-5	Sequence 5, Appl
c 110	3	30.0	10	3	US-08-487-077A-23	Sequence 23, Appl	c 183	3	30.0	15	1	US-08-643-886-5	Sequence 17, Appl
c 111	3	30.0	10	3	US-08-726-807B-47	Sequence 47, Appl	c 184	3	30.0	15	1	US-08-643-886-17	Sequence 17, Appl
c 112	3	30.0	10	3	US-08-726-807B-47	Sequence 47, Appl	c 185	3	30.0	15	2	US-08-643-886-17	Sequence 8, Appl
c 113	3	30.0	10	3	US-08-485-863A-23	Sequence 23, Appl	c 186	3	30.0	15	2	US-08-737-371A-8	Sequence 4, Appl
c 114	3	30.0	10	3	US-08-485-863A-23	Sequence 23, Appl	c 187	3	30.0	15	2	US-08-737-371A-8	Sequence 4, Appl
c 115	3	30.0	10	3	US-08-485-863A-23	Sequence 23, Appl	c 188	3	30.0	15	3	US-08-256-004-4	Sequence 4, Appl
c 116	3	30.0	10	3	US-09-258-367-47	Sequence 47, Appl	c 189	3	30.0	15	4	US-09-461-686-3	Sequence 3, Appl
c 117	3	30.0	10	3	US-09-258-367-47	Sequence 47, Appl	c 190	3	30.0	15	4	US-09-461-686-3	Sequence 3, Appl
c 118	3	30.0	10	3	US-08-972-927-11	Sequence 11, Appl	c 191	3	30.0	15	4	US-09-586-216C-5	Sequence 5, Appl
c 119	3	30.0	10	3	US-08-972-927-11	Sequence 11, Appl	c 192	3	30.0	15	4	US-09-586-216C-5	Sequence 5, Appl
c 120	3	30.0	10	3	US-08-646-301A-11	Sequence 11, Appl	c 193	3	30.0	15	5	PCT-US95-05853-8	Sequence 8, Appl
c 121	3	30.0	10	3	US-08-646-301A-11	Sequence 11, Appl	c 194	3	30.0	15	5	PCT-US95-05853-8	Sequence 8, Appl
c 122	3	30.0	10	3	US-08-485-049D-23	Sequence 23, Appl	c 195	3	30.0	16	1	US-08-486-421-32	Sequence 32, Appl
c 123	3	30.0	10	3	US-08-485-049D-23	Sequence 23, Appl	c 196	3	30.0	16	1	US-08-486-421-32	Sequence 32, Appl
c 124	3	30.0	10	3	US-09-134-246-1	Sequence 1, Appl	c 197	3	30.0	16	1	US-08-643-886-6	Sequence 6, Appl
c 125	3	30.0	10	3	US-09-134-246-1	Sequence 1, Appl	c 198	3	30.0	16	1	US-08-643-886-6	Sequence 6, Appl
c 126	3	30.0	10	3	US-09-546-550-47	Sequence 47, Appl	c 199	3	30.0	16	1	US-08-643-886-18	Sequence 18, Appl
c 127	3	30.0	10	3	US-09-546-550-47	Sequence 47, Appl	c 200	3	30.0	16	1	US-08-643-886-18	Sequence 18, Appl
c 128	3	30.0	10	3	US-09-431-414-47	Sequence 47, Appl	c 201	3	30.0	16	1	US-08-470-911-32	Sequence 32, Appl
c 129	3	30.0	10	3	US-09-431-414-47	Sequence 47, Appl	c 202	3	30.0	16	1	US-08-470-911-32	Sequence 32, Appl
c 130	3	30.0	10	3	US-09-178-115-23	Sequence 23, Appl	c 203	3	30.0	16	2	US-08-486-809-32	Sequence 32, Appl
c 131	3	30.0	10	3	US-09-177-776-23	Sequence 23, Appl	c 204	3	30.0	16	2	US-08-486-809-32	Sequence 32, Appl
c 132	3	30.0	10	3	US-09-177-776-23	Sequence 23, Appl	c 205	3	30.0	16	2	US-08-486-809-32	Sequence 32, Appl
c 133	3	30.0	10	3	US-09-225-670-47	Sequence 47, Appl	c 206	3	30.0	16	3	US-09-012-366-11	Sequence 11, Appl
c 134	3	30.0	10	3	US-09-225-670-47	Sequence 47, Appl	c 207	3	30.0	17	1	US-07-882-838B-11	Sequence 11, Appl
c 135	3	30.0	10	3	US-09-431-349C-47	Sequence 47, Appl	c 208	3	30.0	17	1	US-07-882-838B-11	Sequence 11, Appl
c 136	3	30.0	10	3	US-09-431-349C-47	Sequence 47, Appl	c 209	3	30.0	17	1	US-08-643-886-7	Sequence 7, Appl
c 137	3	30.0	10	4	US-09-122-171D-3	Sequence 3, Appl	c 210	3	30.0	17	1	US-08-643-886-7	Sequence 7, Appl
c 138	3	30.0	10	4	US-09-122-171D-3	Sequence 3, Appl	c 211	3	30.0	17	1	US-08-643-886-19	Sequence 19, Appl
c 139	3	30.0	10	4	US-09-772-719B-23	Sequence 23, Appl	c 212	3	30.0	17	1	US-08-643-886-19	Sequence 19, Appl
c 140	3	30.0	10	4	US-09-772-719B-23	Sequence 23, Appl	c 213	3	30.0	17	3	US-09-302-812-15	Sequence 15, Appl
c 141	3	30.0	10	6	5164316-1	Patent No. 5164316	c 214	3	30.0	17	3	US-09-302-812-15	Sequence 15, Appl
c 142	3	30.0	10	6	5164316-1	Patent No. 5164316	c 215	3	30.0	17	3	US-09-511-477-15	Sequence 15, Appl
c 143	3	30.0	11	1	US-08-643-886-13	Sequence 13, Appl	c 216	3	30.0	17	3	US-09-511-477-15	Sequence 15, Appl
c 144	3	30.0	11	1	US-08-643-886-13	Sequence 13, Appl	c 217	3	30.0	17	3	US-09-511-507-15	Sequence 15, Appl
c 145	3	30.0	12	1	US-08-643-886-2	Sequence 2, Appl	c 218	3	30.0	17	3	US-09-511-507-15	Sequence 15, Appl
c 146	3	30.0	12	1	US-08-643-886-2	Sequence 2, Appl	c 219	3	30.0	17	3	US-09-511-507-15	Sequence 15, Appl
c 147	3	30.0	12	1	US-08-643-886-14	Sequence 14, Appl	c 220	3	30.0	17	4	US-09-457-066-10	Sequence 10, Appl
c 148	3	30.0	12	1	US-08-643-886-14	Sequence 14, Appl	c 221	3	30.0	17	4	US-09-457-066-10	Sequence 10, Appl
c 149	3	30.0	13	1	US-08-235-503B-33	Sequence 33, Appl	c 222	3	30.0	17	4	US-09-564-595D-10	Sequence 10, Appl
c 150	3	30.0	13	1	US-08-235-503B-33	Sequence 33, Appl	c 223	3	30.0	17	4	US-09-564-595D-10	Sequence 10, Appl
c 151	3	30.0	13	1	US-08-643-886-3	Sequence 3, Appl	c 224	3	30.0	17	4	US-09-706-968-10	Sequence 10, Appl
c 152	3	30.0	13	1	US-08-643-886-3	Sequence 3, Appl	c 225	3	30.0	17	4	US-09-706-968-10	Sequence 10, Appl
c 153	3	30.0	13	1	US-08-643-886-3	Sequence 3, Appl	c 226	3	30.0	17	4	US-09-132-368-28	Sequence 28, Appl
c 154	3	30.0	13	1	US-08-643-886-15	Sequence 15, Appl	c 227	3	30.0	17	4	US-09-132-368-28	Sequence 28, Appl
c 155	3	30.0	13	5	PCT-US95-05265-33	Sequence 33, Appl	c 228	3	30.0	17	4	US-09-250-124A-16	Sequence 16, Appl
c 156	3	30.0	13	5	PCT-US95-05265-33	Sequence 33, Appl	c 229	3	30.0	17	4	US-09-250-124A-16	Sequence 16, Appl
c 157	3	30.0	14	1	US-07-882-838E-32	Sequence 32, Appl	c 230	3	30.0	17	4	US-10-043-142-1	Sequence 1, Appl
c 158	3	30.0	14	1	US-07-882-838E-32	Sequence 32, Appl	c 231	3	30.0	17	4	US-10-043-142-1	Sequence 1, Appl
c 159	3	30.0	14	1	US-08-643-886-4	Sequence 4, Appl	c 232	3	30.0	17	4	US-09-806-399-1	Sequence 1, Appl
c 160	3	30.0	14	1	US-08-643-886-4	Sequence 4, Appl	c 233	3	30.0	17	4	US-09-806-399-1	Sequence 1, Appl
c 161	3	30.0	14	1	US-08-643-886-16	Sequence 16, Appl	c 234	3	30.0	17	4	US-09-545-894-18	Sequence 18, Appl
c 162	3	30.0	14	1	US-08-643-886-16	Sequence 16, Appl	c 235	3	30.0	17	4	US-09-545-894-18	Sequence 18, Appl
c 163	3	30.0	14	3	US-08-646-789A-38	Sequence 38, Appl	c 236	3	30.0	17	4	US-09-545-894-19	Sequence 19, Appl
c 164	3	30.0	14	3	US-08-646-789A-38	Sequence 38, Appl	c 237	3	30.0	17	4	US-09-545-894-19	Sequence 19, Appl
c 165	3	30.0	14	3	US-08-646-789A-39	Sequence 39, Appl	c 238	3	30.0	18	1	US-08-643-886-8	Sequence 8, Appl
c 166	3	30.0	14	3	US-08-646-789A-39	Sequence 39, Appl	c 239	3	30.0	18	1	US-08-643-886-8	Sequence 8, Appl
c 167	3	30.0	14	3	US-08-646-301A-8	Sequence 8, Appl	c 240	3	30.0	18	1	US-08-643-886-20	Sequence 20, Appl
c 168	3	30.0	14	3	US-08-646-301A-8	Sequence 8, Appl	c 241	3	30.0	18	1	US-08-643-886-20	Sequence 20, Appl
c 169	3	30.0	14	3	US-09-305-639-7	Sequence 7, Appl	c 242	3	30.0	18	3	US-09-040-025-21	Sequence 21, Appl
c 170	3	30.0	14	3	US-09-305-639-7	Sequence 7, Appl	c 243	3	30.0	18	3	US-09-040-025-21	Sequence 21, Appl
c 171	3	30.0	14	3	US-09-305-384-8	Sequence 8, Appl	c 244	3	30.0	18	3	US-09-040-025-21	Sequence 21, Appl
c 172	3	30.0	14	3	US-09-305-384-8	Sequence 8, Appl	c 245	3	30.0	19	1	US-08-474-542A-136	Sequence 136, App
c 173	3	30.0	14	4	US-09-318-138-22	Sequence 22, Appl	c 246	3	30.0	19	1	US-08-474-542A-136	Sequence 136, App

c 247	3	30.0	19	1	US-08-235-503B-10	Sequence 10, Appl	c 320	3	30.0	23	3	US-09-446-504-48	Sequence 48, Appl
c 248	3	30.0	19	1	US-08-235-503B-11	Sequence 10, Appl	c 321	3	30.0	23	3	US-09-040-025-62	Sequence 62, Appl
c 249	3	30.0	19	1	US-08-235-503B-10	Sequence 11, Appl	c 322	3	30.0	23	3	US-09-040-025-62	Sequence 62, Appl
c 250	3	30.0	19	1	US-08-235-503B-11	Sequence 11, Appl	c 323	3	30.0	23	3	US-09-040-025-64	Sequence 64, Appl
c 251	3	30.0	19	1	US-07-882-838E-10	Sequence 10, Appl	c 324	3	30.0	23	3	US-09-040-025-64	Sequence 64, Appl
c 252	3	30.0	19	1	US-07-882-838E-10	Sequence 10, Appl	c 325	3	30.0	23	3	US-09-712-266-48	Sequence 48, Appl
c 253	3	30.0	19	1	US-08-457-648-136	Sequence 136, App	c 326	3	30.0	23	3	US-09-712-266-48	Sequence 48, Appl
c 254	3	30.0	19	1	US-08-457-648-136	Sequence 136, App	c 327	3	30.0	23	3	US-08-513-974B-15	Sequence 15, Appl
c 255	3	30.0	19	1	US-08-643-886-9	Sequence 9, Appl	c 328	3	30.0	24	3	US-08-513-974B-15	Sequence 15, Appl
c 256	3	30.0	19	1	US-08-643-886-9	Sequence 9, Appl	c 329	3	30.0	24	3	US-08-513-974B-230	Sequence 230, App
c 257	3	30.0	19	4	US-09-672-717-209	Sequence 209, App	c 330	3	30.0	24	3	US-08-513-974B-230	Sequence 230, App
c 258	3	30.0	19	4	US-09-672-717-209	Sequence 209, App	c 331	3	30.0	24	4	US-09-461-436B-15	Sequence 15, Appl
c 259	3	30.0	19	4	US-09-672-717-211	Sequence 211, App	c 332	3	30.0	24	4	US-09-461-436B-15	Sequence 15, Appl
c 260	3	30.0	19	4	US-09-672-717-211	Sequence 211, App	c 333	3	30.0	24	4	US-09-418-980-78	Sequence 78, Appl
c 261	3	30.0	19	5	PCT-US95-05265-10	Sequence 10, Appl	c 334	3	30.0	24	4	US-09-418-980-78	Sequence 78, Appl
c 262	3	30.0	19	5	PCT-US95-05265-10	Sequence 10, Appl	c 335	3	30.0	25	1	US-07-959-119A-7	Sequence 7, Appl
c 263	3	30.0	19	5	PCT-US95-05265-11	Sequence 11, Appl	c 336	3	30.0	25	1	US-07-959-119A-7	Sequence 7, Appl
c 264	3	30.0	19	5	PCT-US95-05265-11	Sequence 11, Appl	c 337	3	30.0	25	2	US-08-744-722-1	Sequence 1, Appl
c 265	3	30.0	20	1	US-07-940-242A-5	Sequence 5, Appl	c 338	3	30.0	25	2	US-08-744-722-1	Sequence 1, Appl
c 266	3	30.0	20	1	US-07-940-242A-5	Sequence 5, Appl	c 339	3	30.0	25	2	US-08-471-994-6	Sequence 6, Appl
c 267	3	30.0	20	1	US-07-940-242A-7	Sequence 7, Appl	c 340	3	30.0	25	2	US-08-471-994-6	Sequence 6, Appl
c 268	3	30.0	20	1	US-07-940-242A-7	Sequence 7, Appl	c 341	3	30.0	25	3	US-08-979-917A-15	Sequence 15, Appl
c 269	3	30.0	20	1	US-08-474-542A-130	Sequence 130, App	c 342	3	30.0	25	3	US-08-979-917A-15	Sequence 15, Appl
c 270	3	30.0	20	1	US-08-474-542A-130	Sequence 130, App	c 343	3	30.0	25	4	US-09-743-954-4	Sequence 4, Appl
c 271	3	30.0	20	1	US-08-457-648-130	Sequence 130, App	c 344	3	30.0	25	4	US-09-743-954-4	Sequence 4, Appl
c 272	3	30.0	20	1	US-08-457-648-130	Sequence 130, App	c 345	3	30.0	25	4	US-08-397-335-7	Sequence 7, Appl
c 273	3	30.0	20	1	US-08-643-886-10	Sequence 10, Appl	c 346	3	30.0	25	4	US-08-397-335-7	Sequence 7, Appl
c 274	3	30.0	20	1	US-08-643-886-10	Sequence 10, Appl	c 347	3	30.0	25	4	US-08-397-335-7	Sequence 7, Appl
c 275	3	30.0	20	2	US-08-680-326-126	Sequence 126, App	c 348	3	30.0	26	1	US-07-714-131C-343	Sequence 343, App
c 276	3	30.0	20	2	US-08-680-326-126	Sequence 126, App	c 349	3	30.0	26	1	US-07-714-131C-343	Sequence 343, App
c 277	3	30.0	20	4	US-09-132-368-30	Sequence 30, Appl	c 350	3	30.0	26	1	US-07-959-119A-10	Sequence 10, Appl
c 278	3	30.0	20	4	US-09-132-368-30	Sequence 30, Appl	c 351	3	30.0	26	1	US-07-959-119A-10	Sequence 10, Appl
c 279	3	30.0	20	4	US-09-732-615-19	Sequence 19, Appl	c 352	3	30.0	26	1	US-08-412-110-343	Sequence 343, App
c 280	3	30.0	20	4	US-09-732-615-19	Sequence 19, Appl	c 353	3	30.0	26	1	US-08-412-110-343	Sequence 343, App
c 281	3	30.0	20	4	US-10-273-051-19	Sequence 19, Appl	c 354	3	30.0	26	1	US-08-409-442A-343	Sequence 343, App
c 282	3	30.0	21	1	US-08-474-542A-298	Sequence 298, App	c 355	3	30.0	26	2	US-08-409-442A-343	Sequence 343, App
c 283	3	30.0	21	1	US-08-474-542A-298	Sequence 298, App	c 356	3	30.0	26	2	US-08-469-609A-343	Sequence 343, App
c 284	3	30.0	21	1	US-08-457-648-298	Sequence 298, App	c 357	3	30.0	26	2	US-08-680-326-5	Sequence 5, Appl
c 285	3	30.0	21	1	US-08-457-648-298	Sequence 298, App	c 358	3	30.0	26	2	US-08-680-326-5	Sequence 5, Appl
c 286	3	30.0	21	1	US-08-457-648-298	Sequence 298, App	c 359	3	30.0	26	2	US-08-680-326-6	Sequence 6, Appl
c 287	3	30.0	21	2	US-08-632-598-10	Sequence 10, Appl	c 360	3	30.0	26	2	US-08-680-326-6	Sequence 6, Appl
c 288	3	30.0	21	2	US-08-632-598-10	Sequence 10, Appl	c 361	3	30.0	26	2	US-08-906-443-2	Sequence 2, Appl
c 289	3	30.0	21	3	US-09-040-025-76	Sequence 76, Appl	c 362	3	30.0	26	3	US-08-906-443-2	Sequence 2, Appl
c 290	3	30.0	21	3	US-09-040-025-76	Sequence 76, Appl	c 363	3	30.0	26	3	US-09-143-190-343	Sequence 343, App
c 291	3	30.0	21	3	US-09-040-025-76	Sequence 76, Appl	c 364	3	30.0	26	3	US-09-143-190-343	Sequence 343, App
c 292	3	30.0	21	3	US-09-040-025-78	Sequence 78, Appl	c 365	3	30.0	26	3	US-08-154-364-13	Sequence 13, Appl
c 293	3	30.0	21	3	US-09-040-025-78	Sequence 78, Appl	c 366	3	30.0	26	3	US-08-154-364-13	Sequence 13, Appl
c 294	3	30.0	21	3	US-09-040-025-107	Sequence 107, App	c 367	3	30.0	26	3	US-08-973-124-269	Sequence 269, App
c 295	3	30.0	21	3	US-09-040-025-107	Sequence 107, App	c 368	3	30.0	26	3	US-08-973-124-269	Sequence 269, App
c 296	3	30.0	21	3	US-09-040-025-109	Sequence 109, App	c 369	3	30.0	26	3	US-09-502-344-343	Sequence 343, App
c 297	3	30.0	21	3	US-09-231-240-10	Sequence 10, Appl	c 370	3	30.0	26	3	US-09-502-344-343	Sequence 343, App
c 298	3	30.0	21	3	US-09-231-240-10	Sequence 10, Appl	c 371	3	30.0	26	4	US-08-397-335-10	Sequence 10, Appl
c 299	3	30.0	21	3	US-09-040-025-76	Sequence 76, Appl	c 372	3	30.0	26	5	US-08-397-335-10	Sequence 10, Appl
c 300	3	30.0	21	3	US-09-040-025-76	Sequence 76, Appl	c 373	3	30.0	26	5	PCT-US96-08014-269	Sequence 269, App
c 301	3	30.0	21	3	US-09-040-025-78	Sequence 78, Appl	c 374	3	30.0	26	5	PCT-US96-08014-269	Sequence 269, App
c 302	3	30.0	21	3	US-09-040-025-78	Sequence 78, Appl	c 375	3	30.0	27	1	US-07-714-131C-337	Sequence 337, App
c 303	3	30.0	21	3	US-09-040-025-107	Sequence 107, App	c 376	3	30.0	27	1	US-07-714-131C-337	Sequence 337, App
c 304	3	30.0	21	3	US-09-040-025-107	Sequence 107, App	c 377	3	30.0	27	1	US-08-412-110-337	Sequence 337, App
c 305	3	30.0	21	3	US-09-040-025-109	Sequence 109, App	c 378	3	30.0	27	1	US-08-412-110-337	Sequence 337, App
c 306	3	30.0	21	3	US-09-040-025-109	Sequence 109, App	c 379	3	30.0	27	1	US-08-409-442A-337	Sequence 337, App
c 307	3	30.0	22	3	US-08-213-741-10	Sequence 10, Appl	c 380	3	30.0	27	1	US-08-409-442A-337	Sequence 337, App
c 308	3	30.0	22	3	US-08-213-741-10	Sequence 10, Appl	c 381	3	30.0	27	2	US-08-469-609A-337	Sequence 337, App
c 309	3	30.0	22	3	US-08-522-336-10	Sequence 10, Appl	c 382	3	30.0	27	2	US-08-469-609A-337	Sequence 337, App
c 310	3	30.0	22	3	US-08-522-336-10	Sequence 10, Appl	c 383	3	30.0	27	3	US-09-143-190-337	Sequence 337, App
c 311	3	30.0	23	2	US-08-193-984-3	Sequence 3, Appl	c 384	3	30.0	27	3	US-09-143-190-337	Sequence 337, App
c 312	3	30.0	23	2	US-08-193-984-3	Sequence 3, Appl	c 385	3	30.0	27	3	US-08-709-838-4	Sequence 4, Appl
c 313	3	30.0	23	2	US-08-896-365-21	Sequence 21, Appl	c 386	3	30.0	27	3	US-08-709-838-4	Sequence 4, Appl
c 314	3	30.0	23	2	US-08-896-365-21	Sequence 21, Appl	c 387	3	30.0	27	3	US-08-829-839-4	Sequence 4, Appl
c 315	3	30.0	23	3	US-09-040-025-62	Sequence 62, Appl	c 388	3	30.0	27	3	US-08-829-839-4	Sequence 4, Appl
c 316	3	30.0	23	3	US-09-040-025-62	Sequence 62, Appl	c 389	3	30.0	27	3	US-08-154-364-6	Sequence 6, Appl
c 317	3	30.0	23	3	US-09-040-025-64	Sequence 64, Appl	c 390	3	30.0	27	3	US-08-154-364-6	Sequence 6, Appl
c 318	3	30.0	23	3	US-09-040-025-64	Sequence 64, Appl	c 391	3	30.0	27	3	US-08-973-124-268	Sequence 268, App
c 319	3	30.0	23	3	US-09-446-504-48	Sequence 48, Appl	c 392	3	30.0	27	3	US-08-973-124-268	Sequence 268, App

393	3	30.0	27	3	US-09-502-344-337	Sequence 337, App	C 466	3	30.0	33	3	US-08-441-971-81	Sequence 81, Appl
C 394	3	30.0	27	3	US-09-502-344-337	Sequence 337, App	467	3	30.0	33	3	US-08-441-971-100	Sequence 100, App
395	3	30.0	27	4	US-08-403-459-59	Sequence 59, Appl	C 468	3	30.0	33	3	US-08-441-971-100	Sequence 100, App
C 396	3	30.0	27	4	US-08-403-459-59	Sequence 59, Appl	469	3	30.0	33	3	US-08-441-971-103	Sequence 103, App
C 397	3	30.0	27	4	US-08-403-459-60	Sequence 60, Appl	C 470	3	30.0	33	3	US-08-441-971-103	Sequence 103, App
C 398	3	30.0	27	4	US-08-403-459-60	Sequence 60, Appl	C 471	3	30.0	33	3	US-08-441-971-113	Sequence 113, App
399	3	30.0	27	4	US-09-033-936-52	Sequence 52, Appl	C 472	3	30.0	33	3	US-08-441-971-113	Sequence 113, App
C 400	3	30.0	27	4	US-09-033-936-52	Sequence 52, Appl	C 473	3	30.0	33	3	US-08-467-023-104	Sequence 104, App
401	3	30.0	27	4	US-09-684-579-9	Sequence 9, Appl	C 474	3	30.0	33	3	US-08-467-023-104	Sequence 104, App
C 402	3	30.0	27	4	US-09-684-579-9	Sequence 9, Appl	C 475	3	30.0	33	3	US-08-451-374-11	Sequence 11, Appl
C 403	3	30.0	27	4	US-09-624-594-4	Sequence 4, Appl	C 476	3	30.0	33	3	US-08-451-374-11	Sequence 11, Appl
C 404	3	30.0	27	4	US-09-624-594-4	Sequence 4, Appl	C 477	3	30.0	33	3	US-08-221-653-81	Sequence 81, Appl
405	3	30.0	27	5	PCT-US96-08014-268	Sequence 268, App	C 478	3	30.0	33	3	US-08-221-653-81	Sequence 81, Appl
C 406	3	30.0	27	5	PCT-US96-08014-268	Sequence 268, App	C 479	3	30.0	33	3	US-08-221-653-100	Sequence 100, App
C 407	3	30.0	28	1	US-07-752-101A-32	Sequence 32, Appl	C 480	3	30.0	33	3	US-08-221-653-103	Sequence 103, App
C 408	3	30.0	28	1	US-07-752-101A-32	Sequence 32, Appl	C 481	3	30.0	33	3	US-08-221-653-103	Sequence 103, App
C 409	3	30.0	29	1	US-07-714-131C-342	Sequence 342, App	C 482	3	30.0	33	3	US-08-221-653-103	Sequence 103, App
C 410	3	30.0	29	1	US-07-714-131C-342	Sequence 342, App	C 483	3	30.0	33	3	US-08-221-653-113	Sequence 113, App
C 411	3	30.0	29	1	US-08-275-225-25	Sequence 25, Appl	C 484	3	30.0	33	3	US-08-221-653-113	Sequence 113, App
C 412	3	30.0	29	1	US-08-275-225-25	Sequence 25, Appl	C 485	3	30.0	33	3	US-08-442-144A-81	Sequence 81, Appl
C 413	3	30.0	29	1	US-08-412-110-342	Sequence 342, App	C 486	3	30.0	33	3	US-08-442-144A-81	Sequence 81, Appl
C 414	3	30.0	29	1	US-08-412-110-342	Sequence 342, App	C 487	3	30.0	33	3	US-08-442-144A-100	Sequence 100, App
C 415	3	30.0	29	1	US-08-409-442A-342	Sequence 342, App	C 488	3	30.0	33	3	US-08-442-144A-100	Sequence 100, App
C 416	3	30.0	29	1	US-08-409-442A-342	Sequence 342, App	C 489	3	30.0	33	3	US-08-442-144A-103	Sequence 103, App
C 417	3	30.0	29	2	US-08-469-609A-342	Sequence 342, App	C 490	3	30.0	33	3	US-08-442-144A-103	Sequence 103, App
C 418	3	30.0	29	2	US-08-469-609A-342	Sequence 342, App	C 491	3	30.0	33	3	US-08-442-144A-113	Sequence 113, App
C 419	3	30.0	29	3	US-09-143-190-342	Sequence 342, App	C 492	3	30.0	33	3	US-08-442-144A-113	Sequence 113, App
C 420	3	30.0	29	3	US-09-143-190-342	Sequence 342, App	C 493	3	30.0	33	3	US-08-935-268A-11	Sequence 11, Appl
C 421	3	30.0	29	3	US-09-502-344-342	Sequence 342, App	C 494	3	30.0	33	3	US-08-935-268A-11	Sequence 11, Appl
C 422	3	30.0	29	3	US-09-502-344-342	Sequence 342, App	C 495	3	30.0	33	3	US-08-441-970-81	Sequence 81, Appl
C 423	3	30.0	29	4	US-09-813-781-104	Sequence 104, App	C 496	3	30.0	33	3	US-08-441-970-81	Sequence 81, Appl
C 424	3	30.0	29	4	US-09-813-781-104	Sequence 104, App	C 497	3	30.0	33	3	US-08-441-970-81	Sequence 81, Appl
C 425	3	30.0	30	1	US-08-186-229-32	Sequence 32, Appl	C 498	3	30.0	33	3	US-08-441-970-100	Sequence 100, App
C 426	3	30.0	30	1	US-08-186-229-32	Sequence 32, Appl	C 499	3	30.0	33	3	US-08-441-970-100	Sequence 100, App
C 427	3	30.0	30	2	US-08-470-124-32	Sequence 32, Appl	C 500	3	30.0	33	3	US-08-441-970-103	Sequence 103, App
C 428	3	30.0	30	2	US-08-470-124-32	Sequence 32, Appl	C 501	3	30.0	33	3	US-08-441-970-103	Sequence 103, App
C 429	3	30.0	30	4	US-09-671-089-36	Sequence 36, Appl	C 502	3	30.0	33	3	US-08-441-970-113	Sequence 113, App
C 430	3	30.0	30	4	US-09-671-089-36	Sequence 36, Appl	C 503	3	30.0	33	3	US-08-441-970-113	Sequence 113, App
C 431	3	30.0	31	1	US-08-086-428B-112	Sequence 112, App	C 504	3	30.0	33	3	US-08-169-715-5	Sequence 5, Appl
C 432	3	30.0	31	1	US-08-086-428B-112	Sequence 112, App	C 505	3	30.0	33	3	US-08-169-715-5	Sequence 5, Appl
C 433	3	30.0	31	2	US-08-086-428B-112	Sequence 112, App	C 506	3	30.0	33	3	US-08-169-715-19	Sequence 19, Appl
C 434	3	30.0	31	2	US-08-468-570-112	Sequence 112, App	C 507	3	30.0	33	3	US-08-169-715-19	Sequence 19, Appl
C 435	3	30.0	31	2	US-08-468-570-112	Sequence 112, App	C 508	3	30.0	33	3	US-08-169-715-59	Sequence 59, Appl
C 436	3	30.0	31	2	US-08-290-665A-216	Sequence 216, App	C 509	3	30.0	33	3	US-08-169-715-59	Sequence 59, Appl
C 437	3	30.0	31	2	US-08-290-665A-216	Sequence 216, App	C 510	3	30.0	33	3	US-08-452-223-11	Sequence 11, Appl
C 438	3	30.0	31	4	US-08-466-601A-112	Sequence 112, App	C 511	3	30.0	33	3	US-08-452-223-11	Sequence 11, Appl
C 439	3	30.0	31	5	PCT-US95-10398-216	Sequence 216, App	C 512	3	30.0	33	3	US-09-671-089-35	Sequence 35, Appl
C 440	3	30.0	31	5	PCT-US95-10398-216	Sequence 216, App	C 513	3	30.0	33	4	US-09-671-089-35	Sequence 35, Appl
C 441	3	30.0	33	1	US-08-138-608-7	Sequence 7, Appl	C 514	3	30.0	34	3	US-08-814-412-24	Sequence 24, Appl
C 442	3	30.0	33	1	US-08-138-608-7	Sequence 7, Appl	C 515	3	30.0	34	3	US-08-814-412-24	Sequence 24, Appl
C 443	3	30.0	33	1	US-08-138-608-11	Sequence 11, Appl	C 516	3	30.0	34	3	US-09-232-477-13	Sequence 13, Appl
C 444	3	30.0	33	1	US-08-138-608-11	Sequence 11, Appl	C 517	3	30.0	34	3	US-09-232-477-13	Sequence 13, Appl
C 445	3	30.0	33	1	US-08-438-639-6	Sequence 6, Appl	C 518	3	30.0	34	4	US-09-784-982-13	Sequence 13, Appl
C 446	3	30.0	33	1	US-08-438-639-6	Sequence 6, Appl	C 519	3	30.0	35	4	US-09-784-982-13	Sequence 13, Appl
C 447	3	30.0	33	1	US-08-438-639-25	Sequence 25, Appl	C 520	3	30.0	35	3	US-09-363-189B-9	Sequence 9, Appl
C 448	3	30.0	33	1	US-08-438-639-25	Sequence 25, Appl	C 521	3	30.0	35	3	US-09-363-189B-9	Sequence 9, Appl
C 449	3	30.0	33	1	US-08-438-639-28	Sequence 28, Appl	C 522	3	30.0	36	1	US-08-482-882-40	Sequence 40, Appl
C 450	3	30.0	33	1	US-08-438-639-28	Sequence 28, Appl	C 523	3	30.0	36	1	US-08-482-882-40	Sequence 40, Appl
C 451	3	30.0	33	1	US-08-438-639-38	Sequence 38, Appl	C 524	3	30.0	36	1	US-08-483-389-40	Sequence 40, Appl
C 452	3	30.0	33	1	US-08-438-639-38	Sequence 38, Appl	C 525	3	30.0	36	1	US-08-483-389-40	Sequence 40, Appl
C 453	3	30.0	33	1	US-07-813-338A-6	Sequence 6, Appl	C 526	3	30.0	36	2	US-08-487-113D-40	Sequence 40, Appl
C 454	3	30.0	33	1	US-07-813-338A-6	Sequence 6, Appl	C 527	3	30.0	36	2	US-08-487-113D-40	Sequence 40, Appl
C 455	3	30.0	33	1	US-07-813-338A-25	Sequence 25, Appl	C 528	3	30.0	36	2	US-08-726-528A-2	Sequence 2, Appl
C 456	3	30.0	33	1	US-07-813-338A-25	Sequence 25, Appl	C 529	3	30.0	36	2	US-08-726-528A-2	Sequence 2, Appl
C 457	3	30.0	33	1	US-07-813-338A-28	Sequence 28, Appl	C 530	3	30.0	36	2	US-08-785-571-3	Sequence 3, Appl
C 458	3	30.0	33	1	US-07-813-338A-28	Sequence 28, Appl	C 531	3	30.0	36	2	US-08-785-571-3	Sequence 3, Appl
C 459	3	30.0	33	1	US-07-813-338A-38	Sequence 38, Appl	C 532	3	30.0	36	2	US-08-473-503-40	Sequence 40, Appl
C 460	3	30.0	33	1	US-07-813-338A-38	Sequence 38, Appl	C 533	3	30.0	36	2	US-08-473-503-40	Sequence 40, Appl
C 461	3	30.0	33	2	US-08-452-242-11	Sequence 11, Appl	C 534	3	30.0	36	2	US-08-483-932-40	Sequence 40, Appl
C 462	3	30.0	33	2	US-08-452-242-11	Sequence 11, Appl	C 535	3	30.0	36	2	US-08-483-932-40	Sequence 40, Appl
C 463	3	30.0	33	3	US-08-453-176A-11	Sequence 11, Appl	C 536	3	30.0	36	2	US-08-720-420A-40	Sequence 40, Appl
C 464	3	30.0	33	3	US-08-453-176A-11	Sequence 11, Appl	C 537	3	30.0	36	2	US-08-720-420A-40	Sequence 40, Appl
C 465	3	30.0	33	3	US-08-441-971-81	Sequence 81, Appl	C 538	3	30.0	36	3	US-08-714-017-40	Sequence 40, Appl

539	3	30.0	3	US-08-475-680-40	Sequence 40, Appl	c 612	3	30.0	61	3	US-08-952-793-377	Sequence 377, App
c 540	3	30.0	36	US-08-475-680-40	Sequence 40, Appl	613	3	30.0	61	4	US-09-849-928-377	Sequence 377, App
541	3	30.0	36	PCT-US93-06734-3	Sequence 3, Appli	c 614	3	30.0	61	4	US-09-849-928-377	Sequence 377, App
c 542	3	30.0	36	PCT-US93-06734-3	Sequence 3, Appli	615	3	30.0	61	4	US-09-621-976-14754	Sequence 14754, A
543	3	30.0	36	PCT-US94-14106-26	Sequence 26, Appl	c 616	3	30.0	61	4	US-09-621-976-14754	Sequence 14754, A
c 544	3	30.0	36	PCT-US94-14106-26	Sequence 26, Appl	617	3	30.0	61	5	PCT-US96-09455A-377	Sequence 377, App
545	3	30.0	37	US-08-388-672A-5	Sequence 5, Appli	c 618	3	30.0	61	5	PCT-US96-09455A-377	Sequence 377, App
c 546	3	30.0	37	US-08-388-672A-5	Sequence 5, Appli	619	3	30.0	63	4	US-09-069-827A-17	Sequence 17, Appl
547	3	30.0	37	US-09-080-554-5	Sequence 5, Appli	c 620	3	30.0	64	4	US-09-069-827A-17	Sequence 17, Appl
c 548	3	30.0	37	US-09-080-554-5	Sequence 5, Appli	621	3	30.0	64	4	US-09-513-999C-25672	Sequence 25672, A
549	3	30.0	38	US-08-814-412-32	Sequence 32, Appl	c 622	3	30.0	64	4	US-09-513-999C-25672	Sequence 25672, A
c 550	3	30.0	38	US-08-814-412-32	Sequence 32, Appl	623	3	30.0	68	4	US-09-513-999C-16627	Sequence 16627, A
551	3	30.0	38	US-09-617-594A-13	Sequence 13, Appl	c 624	3	30.0	68	4	US-09-513-999C-16627	Sequence 16627, A
c 552	3	30.0	38	US-09-617-594A-13	Sequence 13, Appl	625	3	30.0	69	3	US-09-269-911A-7	Sequence 7, Appli
553	3	30.0	39	US-08-485-359-5	Sequence 5, Appli	c 626	3	30.0	69	3	US-09-269-911A-7	Sequence 7, Appli
c 554	3	30.0	39	US-08-485-359-5	Sequence 5, Appli	627	3	30.0	69	3	US-09-269-911A-8	Sequence 8, Appli
555	3	30.0	39	US-08-569-594-5	Sequence 5, Appli	c 628	3	30.0	69	3	US-09-269-911A-8	Sequence 8, Appli
c 556	3	30.0	39	US-08-569-594-5	Sequence 5, Appli	629	3	30.0	70	3	US-08-952-793-369	Sequence 369, App
557	3	30.0	39	US-08-444-644-2	Sequence 2, Appli	c 630	3	30.0	70	3	US-08-952-793-369	Sequence 369, App
c 558	3	30.0	39	US-08-444-644-2	Sequence 2, Appli	631	3	30.0	70	4	US-09-849-928-369	Sequence 369, App
559	3	30.0	39	US-08-444-644-6	Sequence 6, Appli	c 632	3	30.0	70	4	US-09-849-928-369	Sequence 369, App
c 560	3	30.0	39	US-08-444-644-6	Sequence 6, Appli	633	3	30.0	70	5	PCT-US96-09455A-369	Sequence 369, App
561	3	30.0	39	US-08-232-246A-2	Sequence 2, Appli	c 634	3	30.0	70	5	PCT-US96-09455A-369	Sequence 369, App
c 562	3	30.0	39	US-08-232-246A-2	Sequence 2, Appli	635	3	30.0	71	3	US-08-952-793-382	Sequence 382, App
563	3	30.0	39	US-08-232-246A-6	Sequence 6, Appli	c 636	3	30.0	71	3	US-08-952-793-382	Sequence 382, App
c 564	3	30.0	39	US-08-232-246A-6	Sequence 6, Appli	637	3	30.0	71	4	US-09-849-928-382	Sequence 382, App
565	3	30.0	39	US-09-564-329A-26	Sequence 26, Appl	c 638	3	30.0	71	4	US-09-849-928-382	Sequence 382, App
c 566	3	30.0	39	US-09-564-329A-26	Sequence 26, Appl	639	3	30.0	71	4	US-09-513-999C-27432	Sequence 27432, A
567	3	30.0	39	US-09-963-620-26	Sequence 26, Appl	c 640	3	30.0	71	4	US-09-513-999C-27432	Sequence 27432, A
c 568	3	30.0	39	US-09-963-620-26	Sequence 26, Appl	641	3	30.0	71	5	PCT-US96-09455A-382	Sequence 382, App
569	3	30.0	39	US-09-855-632-26	Sequence 26, Appl	c 642	3	30.0	71	5	PCT-US96-09455A-382	Sequence 382, App
c 570	3	30.0	39	US-09-855-632-26	Sequence 26, Appl	643	3	30.0	73	4	US-09-513-999C-19180	Sequence 19180, A
571	3	30.0	39	PCT-US96-08815-5	Sequence 5, Appli	c 644	3	30.0	73	4	US-09-513-999C-19180	Sequence 19180, A
c 572	3	30.0	39	PCT-US96-08815-5	Sequence 5, Appli	645	3	30.0	73	4	US-09-513-999C-25699	Sequence 25699, A
573	3	30.0	42	US-08-933-983-23	Sequence 23, Appl	c 646	3	30.0	73	4	US-09-513-999C-25699	Sequence 25699, A
c 574	3	30.0	42	US-08-933-983-23	Sequence 23, Appl	647	3	30.0	81	4	US-09-603-663-34	Sequence 34, Appl
575	3	30.0	42	US-09-502-653-25	Sequence 25, Appl	c 648	3	30.0	81	4	US-09-603-663-34	Sequence 34, Appl
c 576	3	30.0	42	US-09-502-653-25	Sequence 25, Appl	649	3	30.0	81	4	US-09-603-658-34	Sequence 34, Appl
577	3	30.0	45	US-08-987-943-6	Sequence 6, Appli	c 650	3	30.0	81	4	US-09-603-658-34	Sequence 34, Appl
c 578	3	30.0	45	US-08-987-943-6	Sequence 6, Appli	651	3	30.0	81	4	US-09-602-373A-34	Sequence 34, Appl
579	3	30.0	45	US-08-987-943-7	Sequence 7, Appli	c 652	3	30.0	81	4	US-09-602-373A-34	Sequence 34, Appl
c 580	3	30.0	45	US-08-987-943-7	Sequence 7, Appli	653	3	30.0	81	4	US-09-703-399A-36	Sequence 36, Appl
581	3	30.0	45	US-08-987-943-11	Sequence 11, Appl	c 654	3	30.0	81	4	US-09-703-399A-36	Sequence 36, Appl
c 582	3	30.0	45	US-08-987-943-11	Sequence 11, Appl	655	3	30.0	84	4	US-09-603-663-61	Sequence 61, Appl
583	3	30.0	47	US-09-422-978-3789	Sequence 3789, Ap	c 656	3	30.0	84	4	US-09-603-663-61	Sequence 61, Appl
c 584	3	30.0	47	US-09-422-978-3789	Sequence 3789, Ap	657	3	30.0	84	4	US-09-603-658-61	Sequence 61, Appl
585	3	30.0	48	US-08-230-002-8	Sequence 8, Appli	c 658	3	30.0	84	4	US-09-603-658-61	Sequence 61, Appl
c 586	3	30.0	48	US-08-230-002-8	Sequence 8, Appli	659	3	30.0	84	4	US-09-602-373A-61	Sequence 61, Appl
587	3	30.0	48	US-08-678-854-8	Sequence 8, Appli	c 660	3	30.0	84	4	US-09-602-373A-61	Sequence 61, Appl
c 588	3	30.0	48	US-08-678-854-8	Sequence 8, Appli	661	3	30.0	84	4	US-09-703-399A-58	Sequence 58, Appl
589	3	30.0	48	US-09-300-008B-63	Sequence 63, Appl	c 662	3	30.0	84	4	US-09-703-399A-58	Sequence 58, Appl
c 590	3	30.0	48	US-09-300-008B-63	Sequence 63, Appl	663	3	30.0	84	4	US-09-513-999C-25247	Sequence 25247, A
591	3	30.0	50	US-09-508-930D-32	Sequence 32, Appl	c 664	3	30.0	84	4	US-09-513-999C-25247	Sequence 25247, A
c 592	3	30.0	50	US-09-508-930D-32	Sequence 32, Appl	665	3	30.0	85	4	US-09-621-976-13884	Sequence 13884, A
593	3	30.0	51	US-09-546-934-30	Sequence 30, Appl	c 666	3	30.0	85	4	US-09-621-976-13884	Sequence 13884, A
c 594	3	30.0	51	US-09-546-934-30	Sequence 30, Appl	667	3	30.0	87	4	US-09-513-999C-18169	Sequence 18169, A
595	3	30.0	51	US-09-513-999C-27635	Sequence 27635, A	c 668	3	30.0	87	4	US-09-513-999C-18169	Sequence 18169, A
c 596	3	30.0	51	US-09-513-999C-27635	Sequence 27635, A	669	3	30.0	91	4	US-09-328-750A-5	Sequence 5, Appli
597	3	30.0	58	US-09-621-976-8641	Sequence 8641, Ap	c 670	3	30.0	91	4	US-09-328-750A-5	Sequence 5, Appli
c 598	3	30.0	58	US-09-621-976-8641	Sequence 8641, Ap	671	3	30.0	92	2	US-08-353-372A-16	Sequence 16, Appl
599	3	30.0	58	US-09-513-999C-30029	Sequence 30029, A	c 672	3	30.0	92	2	US-08-353-372A-16	Sequence 16, Appl
c 600	3	30.0	58	US-09-513-999C-30029	Sequence 30029, A	673	3	30.0	92	4	US-09-513-999C-18840	Sequence 18840, A
601	3	30.0	59	US-08-327-525A-14	Sequence 14, Appl	c 674	3	30.0	92	4	US-09-513-999C-18840	Sequence 18840, A
c 602	3	30.0	59	US-08-327-525A-14	Sequence 14, Appl	675	3	30.0	96	3	US-09-240-078-28	Sequence 28, Appl
603	3	30.0	59	US-08-531-137B-14	Sequence 14, Appl	c 676	3	30.0	96	3	US-09-240-078-28	Sequence 28, Appl
c 604	3	30.0	59	US-08-531-137B-14	Sequence 14, Appl	677	3	30.0	96	3	US-09-240-078-29	Sequence 29, Appl
605	3	30.0	59	US-09-158-765-14	Sequence 14, Appl	c 678	3	30.0	96	3	US-09-240-078-29	Sequence 29, Appl
c 606	3	30.0	59	US-09-158-765-14	Sequence 14, Appl	679	3	30.0	96	3	US-09-240-078-31	Sequence 31, Appl
607	3	30.0	59	US-09-796-071-14	Sequence 14, Appl	c 680	3	30.0	96	3	US-09-240-078-31	Sequence 31, Appl
c 608	3	30.0	59	US-09-796-071-14	Sequence 14, Appl	681	3	30.0	97	3	US-08-952-793-272	Sequence 272, App
609	3	30.0	59	US-09-049-805-14	Sequence 14, Appl	c 682	3	30.0	97	3	US-08-952-793-272	Sequence 272, App
c 610	3	30.0	59	US-09-049-805-14	Sequence 14, Appl	683	3	30.0	97	4	US-09-849-928-272	Sequence 272, App
611	3	30.0	61	US-08-952-793-377	Sequence 377, App	c 684	3	30.0	97	4	US-09-849-928-272	Sequence 272, App

685	3	30.0	97	4	US-09-513-999C-30390	Sequence 30390, A	c 758	2	20.0	7	3	US-09-134-246-2	Sequence 2, Appl
686	3	30.0	97	4	US-09-513-999C-30390	Sequence 30390, A	759	2	20.0	7	3	US-09-286-098-102	Sequence 102, App
687	3	30.0	97	5	PCT-US96-09455A-272	Sequence 272, App	c 760	2	20.0	7	3	US-09-286-098-102	Sequence 102, App
688	3	30.0	97	5	PCT-US96-09455A-272	Sequence 272, App	c 761	2	20.0	7	4	US-09-325-193A-88	Sequence 88, Appl
689	3	30.0	98	4	US-09-513-999C-20023	Sequence 20023, A	c 762	2	20.0	7	4	US-09-325-193A-88	Sequence 88, Appl
690	3	30.0	98	4	US-09-513-999C-20023	Sequence 20023, A	c 763	2	20.0	7	4	US-09-857-316-1	Sequence 1, Appl
691	3	30.0	98	4	US-09-513-999C-34152	Sequence 34152, A	c 764	2	20.0	7	4	US-09-857-316-1	Sequence 1, Appl
692	3	30.0	98	4	US-09-513-999C-34152	Sequence 34152, A	c 765	2	20.0	7	4	US-09-857-316-1	Sequence 1, Appl
693	3	30.0	100	4	US-09-513-999C-34152	Sequence 34152, A	c 766	2	20.0	7	4	US-09-641-540-21	Sequence 21, Appl
694	3	30.0	100	4	US-09-513-999C-29839	Sequence 29839, A	c 767	2	20.0	7	4	US-09-641-540-21	Sequence 21, Appl
695	2	20.0	4	1	US-08-368-071-5	Sequence 5, Appl	c 768	2	20.0	7	5	PCT-US94-05659-13	Sequence 13, Appl
696	2	20.0	4	1	US-08-368-071-5	Sequence 5, Appl	c 769	2	20.0	7	5	PCT-US94-05659-13	Sequence 13, Appl
697	2	20.0	4	1	US-08-458-181-5	Sequence 5, Appl	c 770	2	20.0	7	5	PCT-US95-04092-12	Sequence 12, Appl
698	2	20.0	4	1	US-08-458-181-5	Sequence 5, Appl	c 771	2	20.0	7	5	PCT-US95-04092-12	Sequence 12, Appl
699	2	20.0	4	1	US-08-458-181-5	Sequence 5, Appl	c 772	2	20.0	8	1	US-08-347-826A-13	Sequence 13, Appl
700	2	20.0	4	5	PCT-US93-02172-5	Sequence 5, Appl	c 773	2	20.0	8	1	US-08-347-826A-13	Sequence 13, Appl
701	2	20.0	4	5	PCT-US93-02172-5	Sequence 5, Appl	c 774	2	20.0	8	2	US-08-903-624-17	Sequence 17, Appl
702	2	20.0	5	1	US-07-630-288A-1	Sequence 1, Appl	c 775	2	20.0	8	2	US-08-903-624-17	Sequence 17, Appl
703	2	20.0	5	1	US-07-630-288A-1	Sequence 1, Appl	c 776	2	20.0	8	3	US-08-646-301A-10	Sequence 10, Appl
704	2	20.0	5	1	US-07-630-288A-43	Sequence 43, Appl	c 777	2	20.0	8	3	US-08-646-301A-10	Sequence 10, Appl
705	2	20.0	5	1	US-07-630-288A-43	Sequence 43, Appl	c 778	2	20.0	8	3	US-09-030-701-3	Sequence 3, Appl
706	2	20.0	5	1	US-08-468-049-1	Sequence 1, Appl	c 779	2	20.0	8	3	US-09-030-701-3	Sequence 3, Appl
707	2	20.0	5	1	US-08-468-049-1	Sequence 1, Appl	c 780	2	20.0	8	4	US-08-705-477B-106	Sequence 106, App
708	2	20.0	5	1	US-08-468-049-43	Sequence 43, Appl	c 781	2	20.0	8	4	US-08-705-477B-106	Sequence 106, App
709	2	20.0	5	1	US-08-468-049-43	Sequence 43, Appl	c 782	2	20.0	8	4	US-08-705-477B-108	Sequence 108, App
710	2	20.0	5	4	US-09-933-313B-5	Sequence 5, Appl	c 783	2	20.0	8	4	US-08-705-477B-108	Sequence 108, App
711	2	20.0	5	4	US-09-933-313B-5	Sequence 5, Appl	c 784	2	20.0	8	4	US-09-601-537-21	Sequence 21, Appl
712	2	20.0	5	4	US-10-037-927B-7	Sequence 7, Appl	c 785	2	20.0	8	4	US-09-601-537-21	Sequence 21, Appl
713	2	20.0	5	4	US-10-037-927B-7	Sequence 7, Appl	c 786	2	20.0	8	4	US-09-915-060A-19	Sequence 19, Appl
714	2	20.0	5	4	US-09-975-413A-7	Sequence 7, Appl	c 787	2	20.0	8	4	US-09-915-060A-19	Sequence 19, Appl
715	2	20.0	5	4	US-09-957-005-6	Sequence 6, Appl	c 788	2	20.0	9	1	US-08-566-037A-1	Sequence 1, Appl
716	2	20.0	5	4	US-09-957-005-6	Sequence 6, Appl	c 789	2	20.0	9	1	US-08-566-037A-1	Sequence 1, Appl
717	2	20.0	5	4	US-09-510-238A-4	Sequence 4, Appl	c 790	2	20.0	9	1	US-08-566-037A-6	Sequence 6, Appl
718	2	20.0	5	4	US-09-510-238A-4	Sequence 4, Appl	c 791	2	20.0	9	1	US-08-566-037A-6	Sequence 6, Appl
719	2	20.0	5	4	US-09-966-997-8	Sequence 8, Appl	c 792	2	20.0	9	1	US-08-153-848-20	Sequence 20, Appl
720	2	20.0	5	4	US-09-966-997-8	Sequence 8, Appl	c 793	2	20.0	9	1	US-08-153-848-20	Sequence 20, Appl
721	2	20.0	5	4	US-08-169-950-4	Sequence 4, Appl	c 794	2	20.0	9	1	US-08-488-015B-20	Sequence 20, Appl
722	2	20.0	6	1	US-08-169-950-4	Sequence 4, Appl	c 795	2	20.0	9	1	US-08-488-015B-20	Sequence 20, Appl
723	2	20.0	6	1	US-08-133-179-7	Sequence 7, Appl	c 796	2	20.0	9	1	US-08-667-023-12	Sequence 12, Appl
724	2	20.0	6	1	US-08-133-179-7	Sequence 7, Appl	c 797	2	20.0	9	1	US-08-667-023-12	Sequence 12, Appl
725	2	20.0	6	1	US-08-692-825-19	Sequence 19, Appl	c 798	2	20.0	9	2	US-08-224-482-10	Sequence 10, Appl
726	2	20.0	6	2	US-08-692-825-19	Sequence 19, Appl	c 799	2	20.0	9	2	US-08-224-482-10	Sequence 10, Appl
727	2	20.0	6	2	US-08-468-819-25	Sequence 25, Appl	c 800	2	20.0	9	2	US-08-590-571-66	Sequence 66, Appl
728	2	20.0	6	2	US-08-468-819-25	Sequence 25, Appl	c 801	2	20.0	9	2	US-08-590-571-66	Sequence 66, Appl
729	2	20.0	6	3	US-09-037-135-2	Sequence 2, Appl	c 802	2	20.0	9	2	US-08-480-473B-26	Sequence 26, Appl
730	2	20.0	6	3	US-09-037-135-2	Sequence 2, Appl	c 803	2	20.0	9	2	US-08-480-473B-26	Sequence 26, Appl
731	2	20.0	6	3	US-08-895-495-19	Sequence 19, Appl	c 804	2	20.0	9	3	US-08-915-213-26	Sequence 26, Appl
732	2	20.0	6	3	US-08-895-495-19	Sequence 19, Appl	c 805	2	20.0	9	3	US-08-915-213-26	Sequence 26, Appl
733	2	20.0	6	3	US-09-404-670-1	Sequence 1, Appl	c 806	2	20.0	9	3	US-08-335-865J-12	Sequence 12, Appl
734	2	20.0	6	3	US-09-404-670-1	Sequence 1, Appl	c 807	2	20.0	9	3	US-08-335-865J-12	Sequence 12, Appl
735	2	20.0	6	3	US-09-404-671-1	Sequence 1, Appl	c 808	2	20.0	9	3	US-09-299-843A-20	Sequence 20, Appl
736	2	20.0	6	3	US-09-404-671-1	Sequence 1, Appl	c 809	2	20.0	9	3	US-09-299-843A-20	Sequence 20, Appl
737	2	20.0	6	3	US-08-646-301A-12	Sequence 12, Appl	c 810	2	20.0	9	3	US-09-258-367-17	Sequence 17, Appl
738	2	20.0	6	3	US-08-646-301A-12	Sequence 12, Appl	c 811	2	20.0	9	3	US-09-258-367-17	Sequence 17, Appl
739	2	20.0	6	3	US-09-030-701-1	Sequence 1, Appl	c 812	2	20.0	9	3	US-09-258-367-17	Sequence 17, Appl
740	2	20.0	6	3	US-09-030-701-1	Sequence 1, Appl	c 813	2	20.0	9	3	US-08-973-068-55	Sequence 55, Appl
741	2	20.0	6	3	US-09-286-098-101	Sequence 101, App	c 814	2	20.0	9	3	US-08-973-068-55	Sequence 55, Appl
742	2	20.0	6	3	US-09-286-098-101	Sequence 101, App	c 815	2	20.0	9	3	US-09-163-485-16	Sequence 16, Appl
743	2	20.0	6	3	US-09-401-869-1	Sequence 1, Appl	c 816	2	20.0	9	3	US-09-163-485-16	Sequence 16, Appl
744	2	20.0	6	3	US-09-401-869-1	Sequence 1, Appl	c 817	2	20.0	9	3	US-09-546-550-17	Sequence 17, Appl
745	2	20.0	6	3	US-09-401-869-1	Sequence 1, Appl	c 818	2	20.0	9	3	US-09-546-550-17	Sequence 17, Appl
746	2	20.0	6	3	US-09-401-870-1	Sequence 1, Appl	c 819	2	20.0	9	3	US-09-431-414-17	Sequence 17, Appl
747	2	20.0	6	3	US-09-401-870-1	Sequence 1, Appl	c 820	2	20.0	9	3	US-09-431-414-17	Sequence 17, Appl
748	2	20.0	6	3	US-09-404-056-1	Sequence 1, Appl	c 821	2	20.0	9	3	US-09-225-670-17	Sequence 17, Appl
749	2	20.0	6	3	US-09-404-056-1	Sequence 1, Appl	c 822	2	20.0	9	3	US-09-225-670-17	Sequence 17, Appl
750	2	20.0	6	4	US-09-325-193A-87	Sequence 87, Appl	c 823	2	20.0	9	3	US-09-008-097-9	Sequence 9, Appl
751	2	20.0	6	4	US-09-325-193A-87	Sequence 87, Appl	c 824	2	20.0	9	3	US-09-008-097-9	Sequence 9, Appl
752	2	20.0	6	4	US-09-632-538C-10	Sequence 10, Appl	c 825	2	20.0	9	3	US-08-623-428D-61	Sequence 61, Appl
753	2	20.0	6	4	US-09-632-538C-10	Sequence 10, Appl	c 826	2	20.0	9	3	US-08-623-428D-61	Sequence 61, Appl
754	2	20.0	6	4	US-09-213-383-25	Sequence 25, Appl	c 827	2	20.0	9	3	US-08-709-731A-4	Sequence 4, Appl
755	2	20.0	6	4	US-09-213-383-25	Sequence 25, Appl	c 828	2	20.0	9	3	US-08-709-731A-4	Sequence 4, Appl
756	2	20.0	7	2	US-08-853-703A-1	Sequence 1, Appl	c 829	2	20.0	9	3	US-08-431-349C-17	Sequence 17, Appl
757	2	20.0	7	3	US-09-134-246-2	Sequence 2, Appl	c 830	2	20.0	9	3	US-09-431-349C-17	Sequence 17, Appl

831	2	20.0	9	3	US-09-088-337B-20	Sequence 20, Appl	c 904	2	20.0	10	4	US-08-912-951-105	Sequence 105, App
c 832	2	20.0	9	3	US-09-088-337B-20	Sequence 20, Appl	905	2	20.0	10	4	US-09-087-031E-8	Sequence 8, Appl
833	2	20.0	9	4	US-09-305-839-45	Sequence 45, Appl	c 906	2	20.0	10	4	US-09-087-031E-8	Sequence 8, Appl
c 834	2	20.0	9	4	US-09-305-839-45	Sequence 45, Appl	907	2	20.0	10	4	US-08-600-203-6	Sequence 6, Appl
835	2	20.0	9	4	US-09-803-263-13	Sequence 13, Appl	c 908	2	20.0	10	4	US-08-600-203-6	Sequence 6, Appl
c 836	2	20.0	9	4	US-09-803-263-13	Sequence 13, Appl	909	2	20.0	10	4	US-09-849-928-183	Sequence 183, App
837	2	20.0	9	4	US-09-472-667-9	Sequence 9, Appl	c 910	2	20.0	10	4	US-09-849-928-183	Sequence 183, App
c 838	2	20.0	9	4	US-09-472-667-9	Sequence 9, Appl	911	2	20.0	10	4	US-08-705-477E-107	Sequence 107, App
839	2	20.0	9	5	PCT-US93-11153-20	Sequence 20, Appl	c 912	2	20.0	10	4	US-08-705-477E-107	Sequence 107, App
c 840	2	20.0	9	5	PCT-US93-11153-20	Sequence 20, Appl	913	2	20.0	10	4	US-09-548-880B-2	Sequence 2, Appl
841	2	20.0	9	5	PCT-US96-10251-26	Sequence 26, Appl	c 914	2	20.0	10	4	US-09-548-880B-2	Sequence 2, Appl
c 842	2	20.0	9	5	PCT-US96-10251-26	Sequence 26, Appl	915	2	20.0	10	4	US-09-402-181B-105	Sequence 105, App
843	2	20.0	10	1	US-08-235-503B-3	Sequence 3, Appl	c 916	2	20.0	10	4	US-09-402-181B-105	Sequence 105, App
c 844	2	20.0	10	1	US-08-235-503B-3	Sequence 3, Appl	917	2	20.0	10	4	US-09-721-456-105	Sequence 105, App
845	2	20.0	10	1	US-08-351-748-12	Sequence 12, Appl	c 918	2	20.0	10	4	US-09-721-456-105	Sequence 105, App
c 846	2	20.0	10	1	US-08-351-748-12	Sequence 12, Appl	919	2	20.0	10	4	US-08-961-888-5	Sequence 5, Appl
847	2	20.0	10	1	US-08-430-536A-12	Sequence 12, Appl	c 920	2	20.0	10	4	US-08-961-888-5	Sequence 5, Appl
c 848	2	20.0	10	1	US-08-430-536A-12	Sequence 12, Appl	921	2	20.0	10	4	US-08-260-190-20	Sequence 20, Appl
849	2	20.0	10	1	US-08-122-433-14	Sequence 14, Appl	c 922	2	20.0	10	4	US-08-260-190-20	Sequence 20, Appl
c 850	2	20.0	10	1	US-08-122-433-14	Sequence 14, Appl	923	2	20.0	10	4	PCT-US93-02246-12	Sequence 12, Appl
851	2	20.0	10	1	US-08-250-740-36	Sequence 36, Appl	c 924	2	20.0	10	5	PCT-US93-02246-12	Sequence 12, Appl
c 852	2	20.0	10	1	US-08-250-740-36	Sequence 36, Appl	925	2	20.0	10	5	PCT-US93-08386-21	Sequence 21, Appl
853	2	20.0	10	1	US-08-472-255A-170	Sequence 170, App	c 926	2	20.0	10	5	PCT-US93-08386-21	Sequence 21, Appl
c 854	2	20.0	10	1	US-08-472-255A-170	Sequence 170, App	927	2	20.0	10	5	PCT-US94-04361-2	Sequence 2, Appl
855	2	20.0	10	1	US-08-479-724A-170	Sequence 170, App	c 928	2	20.0	10	5	PCT-US94-04361-2	Sequence 2, Appl
c 856	2	20.0	10	1	US-08-479-724A-170	Sequence 170, App	929	2	20.0	10	5	PCT-US95-05265-3	Sequence 3, Appl
857	2	20.0	10	1	US-08-591-989-58	Sequence 58, Appl	c 930	2	20.0	10	5	PCT-US95-05265-3	Sequence 3, Appl
c 858	2	20.0	10	1	US-08-591-989-58	Sequence 58, Appl	931	2	20.0	10	5	PCT-US95-05853-12	Sequence 12, Appl
859	2	20.0	10	1	US-08-414-398-1	Sequence 1, Appl	c 932	2	20.0	10	5	PCT-US95-05853-12	Sequence 12, Appl
c 860	2	20.0	10	1	US-08-414-398-1	Sequence 1, Appl	933	2	20.0	10	5	PCT-US95-05853-13	Sequence 13, Appl
861	2	20.0	10	2	US-08-590-571-14	Sequence 14, Appl	c 934	2	20.0	10	5	PCT-US95-05853-13	Sequence 13, Appl
c 862	2	20.0	10	2	US-08-590-571-14	Sequence 14, Appl	935	2	20.0	10	5	PCT-US95-05853-14	Sequence 14, Appl
863	2	20.0	10	2	US-08-627-151A-19	Sequence 19, Appl	c 936	2	20.0	10	5	PCT-US95-05853-14	Sequence 14, Appl
c 864	2	20.0	10	2	US-08-627-151A-19	Sequence 19, Appl	937	2	20.0	10	5	PCT-US95-05853-14	Sequence 14, Appl
865	2	20.0	10	2	US-08-676-279-30	Sequence 30, Appl	c 938	2	20.0	10	5	PCT-US96-04455A-183	Sequence 183, App
c 866	2	20.0	10	2	US-08-676-279-30	Sequence 30, Appl	939	2	20.0	10	5	PCT-US96-04455A-183	Sequence 183, App
867	2	20.0	10	2	US-08-480-473B-19	Sequence 19, Appl	c 940	2	20.0	10	5	PCT-US96-10251-19	Sequence 19, Appl
c 868	2	20.0	10	2	US-08-480-473B-19	Sequence 19, Appl	941	2	20.0	11	1	US-08-235-503B-21	Sequence 21, Appl
869	2	20.0	10	2	US-08-737-371A-12	Sequence 12, Appl	c 942	2	20.0	11	1	US-08-235-503B-21	Sequence 21, Appl
c 870	2	20.0	10	2	US-08-737-371A-12	Sequence 12, Appl	943	2	20.0	11	1	US-08-358-810A-6	Sequence 6, Appl
871	2	20.0	10	2	US-08-737-371A-13	Sequence 13, Appl	c 944	2	20.0	11	1	US-08-358-810A-6	Sequence 6, Appl
c 872	2	20.0	10	2	US-08-737-371A-13	Sequence 13, Appl	945	2	20.0	11	1	US-08-484-712A-6	Sequence 6, Appl
873	2	20.0	10	2	US-08-737-371A-14	Sequence 14, Appl	c 946	2	20.0	11	1	US-08-484-712A-6	Sequence 6, Appl
c 874	2	20.0	10	2	US-08-737-371A-14	Sequence 14, Appl	947	2	20.0	11	1	US-08-359-295C-2	Sequence 2, Appl
875	2	20.0	10	2	US-08-684-547-12	Sequence 12, Appl	c 948	2	20.0	11	1	US-08-359-295C-2	Sequence 2, Appl
c 876	2	20.0	10	2	US-08-684-547-12	Sequence 12, Appl	949	2	20.0	11	1	US-08-597-495B-21	Sequence 21, Appl
877	2	20.0	10	2	US-08-822-701-6	Sequence 6, Appl	c 950	2	20.0	11	1	US-08-597-495B-21	Sequence 21, Appl
c 878	2	20.0	10	2	US-08-822-701-6	Sequence 6, Appl	951	2	20.0	11	1	US-08-472-255A-121	Sequence 121, App
879	2	20.0	10	2	US-08-927-722-16	Sequence 16, Appl	c 952	2	20.0	11	1	US-08-472-255A-121	Sequence 121, App
c 880	2	20.0	10	2	US-08-927-722-16	Sequence 16, Appl	953	2	20.0	11	1	US-08-479-724A-121	Sequence 121, App
881	2	20.0	10	2	US-08-724-354D-13	Sequence 13, Appl	c 954	2	20.0	11	1	US-08-479-724A-121	Sequence 121, App
c 882	2	20.0	10	2	US-08-724-354D-13	Sequence 13, Appl	955	2	20.0	11	1	US-08-488-015B-14	Sequence 14, Appl
883	2	20.0	10	3	US-08-472-256B-170	Sequence 170, App	c 956	2	20.0	11	1	US-08-488-015B-14	Sequence 14, Appl
c 884	2	20.0	10	3	US-08-472-256B-170	Sequence 170, App	957	2	20.0	11	1	US-08-327-525A-34	Sequence 34, Appl
885	2	20.0	10	3	US-08-915-213-19	Sequence 19, Appl	c 958	2	20.0	11	1	US-08-327-525A-34	Sequence 34, Appl
c 886	2	20.0	10	3	US-08-915-213-19	Sequence 19, Appl	959	2	20.0	11	1	US-08-327-525A-35	Sequence 35, Appl
887	2	20.0	10	3	US-09-270-984A-13	Sequence 13, Appl	c 960	2	20.0	11	1	US-08-327-525A-35	Sequence 35, Appl
c 888	2	20.0	10	3	US-09-270-984A-13	Sequence 13, Appl	961	2	20.0	11	2	US-08-659-453B-3	Sequence 3, Appl
889	2	20.0	10	3	US-08-933-855-6	Sequence 6, Appl	c 962	2	20.0	11	2	US-08-659-453B-3	Sequence 3, Appl
c 890	2	20.0	10	3	US-08-933-855-6	Sequence 6, Appl	963	2	20.0	11	2	US-08-485-105A-2	Sequence 2, Appl
891	2	20.0	10	3	US-08-974-549A-105	Sequence 105, App	c 964	2	20.0	11	2	US-08-485-105A-2	Sequence 2, Appl
c 892	2	20.0	10	3	US-08-974-549A-105	Sequence 105, App	965	2	20.0	11	2	US-08-321-670-7	Sequence 7, Appl
893	2	20.0	10	3	US-09-235-217-19	Sequence 19, Appl	c 966	2	20.0	11	2	US-08-321-670-7	Sequence 7, Appl
c 894	2	20.0	10	3	US-09-235-217-19	Sequence 19, Appl	967	2	20.0	11	2	US-08-583-562B-18	Sequence 18, Appl
895	2	20.0	10	3	US-08-952-793-183	Sequence 183, App	c 968	2	20.0	11	2	US-08-583-562B-18	Sequence 18, Appl
c 896	2	20.0	10	3	US-08-952-793-183	Sequence 183, App	969	2	20.0	11	2	US-08-531-137B-34	Sequence 34, Appl
897	2	20.0	10	3	US-08-623-428D-56	Sequence 56, Appl	c 970	2	20.0	11	2	US-08-531-137B-34	Sequence 34, Appl
c 898	2	20.0	10	3	US-08-623-428D-56	Sequence 56, Appl	971	2	20.0	11	2	US-08-531-137B-35	Sequence 35, Appl
899	2	20.0	10	4	US-08-927-165A-39	Sequence 39, Appl	c 972	2	20.0	11	2	US-08-531-137B-35	Sequence 35, Appl
c 900	2	20.0	10	4	US-08-927-165A-39	Sequence 39, Appl	973	2	20.0	11	3	US-08-472-256B-121	Sequence 121, App
901	2	20.0	10	4	US-09-378-069A-16	Sequence 16, Appl	c 974	2	20.0	11	3	US-08-472-256B-121	Sequence 121, App
c 902	2	20.0	10	4	US-09-378-069A-16	Sequence 16, Appl	975	2	20.0	11	3	US-08-946-138-3	Sequence 3, Appl
903	2	20.0	10	4	US-08-912-951-105	Sequence 105, App	c 976	2	20.0	11	3	US-08-946-138-3	Sequence 3, Appl


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; Patent No. 5744310
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: BAX Promoter Sequence and Screening
; Patent No. 5744310
; TITLE OF INVENTION: Assays for Identifying Agents that Regulate BAX Gene
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,145
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-688-145-3
; Query Match 100.0%; Score 10; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYY 10
Db 1 RRCWGWYY 10

RESULT 4
US-08-688-145-3/c
; Sequence 3, Application US/08688145
; Patent No. 5744310
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; TITLE OF INVENTION: BAX Promoter Sequence and Screening
; Patent No. 5744310
; TITLE OF INVENTION: Assays for Identifying Agents that Regulate BAX Gene
; TITLE OF INVENTION: Expression
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell and Flores
; STREET: 4370 La Jolla Village Drive
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
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; APPLICATION NUMBER: US/08/688,145
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 1951
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-688-145-3
; Query Match 100.0%; Score 10; DB 1; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYY 10
Db 10 RRCWGWYY 1

RESULT 5
US-08-838-844-30
; Sequence 30, Application US/08838844
; Patent No. 5908750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Miyashita, Toshiyuki
; APPLICANT: Hanigai, Masayoshi
; APPLICANT: Hanada, Motoi
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
; TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
; TITLE OF INVENTION: DEATH
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,844
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182,619
; FILING DATE: 14-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,535
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2520
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
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; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-838-844-30

Query Match      100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10
Db 1 RRRCWGYYY 10

RESULT 6
US-08-838-844-30/c
; Sequence 30, Application US/08838844
; Patent No. 5908750
; GENERAL INFORMATION:
; APPLICANT: Reed, John C.
; APPLICANT: Miyashita, Toshiyuki
; APPLICANT: Harigai, Masayoshi
; APPLICANT: Hanada, Motoi
; TITLE OF INVENTION: SCREENING ASSAYS FOR IDENTIFYING AGENTS
; TITLE OF INVENTION: THAT REGULATE THE EXPRESSION OF GENES INVOLVED IN CELL
; TITLE OF INVENTION: DEATH
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESS: Campbell & Flores LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: USA
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,844
; FILING DATE: 11-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/182,619
; FILING DATE: 14-JAN-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/330,535
; FILING DATE: 27-OCT-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Campbell, Cathryn A.
; REGISTRATION NUMBER: 31,815
; REFERENCE/DOCKET NUMBER: P-LJ 2520
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619) 535-9001
; TELEFAX: (619) 535-8949
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-838-844-30

Query Match      100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10
Db 10 RRRCWGYYY 1
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RESULT 7
US-08-299-074A-3
; Sequence 3, Application US/08299074A
; Patent No. 595283
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; TITLE OF INVENTION: BY P53
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,074A
; FILING DATE: 01-SEP-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,758
; FILING DATE: 31-MAR-1992
; APPLICATION NUMBER: 07/715,182
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: linear
US-08-299-074A-3

Query Match      100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10
Db 1 RRRCWGYYY 10

RESULT 8
US-08-299-074A-3/c
; Sequence 3, Application US/08299074A
; Patent No. 595263
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; TITLE OF INVENTION: BY P53
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESS: Banner & Witcoff
; STREET: 1001 G Street, NW
```

;
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,074A
; FILING DATE: 01-SEP-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,758
; FILING DATE: 31-MAR-1992
; APPLICATION NUMBER: 07/715,182
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-299-074A-3

Query Match 100.0%; Score 10; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYY 10
||| |||||
Db 10 RRRCWGYY 1

RESULT 9
US-09-173-914-29/c
; Sequence 29, Application US/09173914
; Patent No. 6171857
; GENERAL INFORMATION:
; APPLICANT: Hendrickson, Eric
; TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
; FILE REFERENCE: B0877/7017/HK
; CURRENT APPLICATION NUMBER: US/09/173,914
; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 60/064,557
; EARLIER FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-173-914-29

Query Match 100.0%; Score 10; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYY 10
||| |||||
Db 1 RRRCWGYY 10

RESULT 10
US-09-173-914-29/c
; Sequence 29, Application US/09173914
; Patent No. 6171857
; GENERAL INFORMATION:
; APPLICANT: Hendrickson, Eric
; TITLE OF INVENTION: A No. 6171857el Leucine Zipper, KARP-1 and
; FILE REFERENCE: B0877/7017/HK
; CURRENT APPLICATION NUMBER: US/09/173,914
; CURRENT FILING DATE: 1998-10-16
; EARLIER APPLICATION NUMBER: 60/064,557
; EARLIER FILING DATE: 1997-10-17
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo Sapiens
US-09-173-914-29

Query Match 100.0%; Score 10; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYY 10
||| |||||
Db 10 RRRCWGYY 1

RESULT 11
US-09-399-773-3
; Sequence 3, Application US/09399773
; Patent No. 6245515
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; TITLE OF INVENTION: BY P53
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/399,773
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/299,074
; FILING DATE:
; APPLICATION NUMBER: 07/715,182
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-399-773-3

Query Match 100.0%; Score 10; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10
| | | | |
Db 1 RRRCWGYY 10

RESULT 12

US-09-399-773-3/c
; Sequence 3, Application US/0399773
; Patent No. 624515

GENERAL INFORMATION:

; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; NUMBER OF SEQUENCES: BY P53
; CORRESPONDENCE ADDRESS: 41
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/399,773
; FILING DATE:

CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/299,074
; FILING DATE:
; APPLICATION NUMBER: 07/715,182
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:

INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-399-773-3

Query Match 100.0%; Score 10; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10
| | | | |
Db 10 RRRCWGYY 1

RESULT 13

US-09-928-385B-24

; Sequence 24, Application US/09928385B
; Patent No. 6544746
; GENERAL INFORMATION:

; APPLICANT: Heyduk, Tomasz
; TITLE OF INVENTION: A Rapid and Sensitive Proximity-Based Assay for the Detection
; TITLE OF INVENTION: and Quantification of DNA Binding Proteins
; FILE REFERENCE: 16153-7963
; CURRENT APPLICATION NUMBER: US/09/928,385B
; CURRENT FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: These sequences were chemically synthesized,
; OTHER INFORMATION: but may also be created via recombinant methods.
US-09-928-385B-24

Query Match 100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10
| | | | |
Db 1 RRRCWGYY 10

RESULT 14

US-09-928-385B-24/c
; Sequence 24, Application US/09928385B
; Patent No. 6544746
; GENERAL INFORMATION:

; APPLICANT: Heyduk, Tomasz
; TITLE OF INVENTION: A Rapid and Sensitive Proximity-Based Assay for the Detection
; TITLE OF INVENTION: and Quantification of DNA Binding Proteins
; FILE REFERENCE: 16153-7963
; CURRENT APPLICATION NUMBER: US/09/928,385B
; CURRENT FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: These sequences were chemically synthesized,
; OTHER INFORMATION: but may also be created via recombinant methods.
US-09-928-385B-24

Query Match 100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYY 10
| | | | |
Db 10 RRRCWGYY 1

RESULT 15

US-08-260-190-21
; Sequence 21, Application US/08260190A
; Patent No. 6774117
; GENERAL INFORMATION:

; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/08/260,190A

```
; CURRENT FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(10)
US-08-260-190-21
```

```
Query Match      100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RRRCWGYYY 10
        |||||
Db       1 RRRCWGYYY 10
```

```
RESULT 16
US-08-260-190-21/c
; Sequence 21, Application US/08260190A
; Patent No. 6774117
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaronir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/08/260,190A
; CURRENT FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(10)
US-08-260-190-21
```

```
Query Match      100.0%; Score 10; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RRRCWGYYY 10
        |||||
Db       10 RRRCWGYYY 1
```

```
RESULT 17
US-09-210-748A-6
; Sequence 6, Application US/09210748A
; Patent No. 6335156
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
```

```
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; FILE REFERENCE: 1107.77810
; CURRENT APPLICATION NUMBER: US/09/210,748A
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/069,416
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-210-748A-6
```

```
Query Match      100.0%; Score 10; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RRRCWGYYY 10
        |||||
Db       1 RRRCWGYYY 10
```

```
RESULT 18
US-09-210-748A-6/c
; Sequence 6, Application US/09210748A
; Patent No. 6335156
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; FILE REFERENCE: 1107.77810
; CURRENT APPLICATION NUMBER: US/09/210,748A
; CURRENT FILING DATE: 1998-12-15
; PRIOR APPLICATION NUMBER: 60/069,416
; PRIOR FILING DATE: 1997-12-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-210-748A-6
```

```
Query Match      100.0%; Score 10; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 RRRCWGYYY 10
        |||||
Db       20 RRRCWGYYY 11
```

```
RESULT 19
US-09-939-581A-6
; Sequence 6, Application US/09939581A
; Patent No. 6740523
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; FILE REFERENCE: 1107.77810
; CURRENT APPLICATION NUMBER: US/09/939,581A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/210,748
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
```

```
/ ORGANISM: Homo sapiens
US-09-939-581A-6
  Query Match      100.0%; Score 10; DB 4; Length 20;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 1 RRCWGWYYY 10

RESULT 20
US-09-939-581A-6/c
; Sequence 6, Application US/09939581A
; Patent No. 6740523
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Helko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; FILE REFERENCE: 1107.77810
; CURRENT APPLICATION NUMBER: US/09/939,581A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/210,748
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-939-581A-6
  Query Match      100.0%; Score 10; DB 4; Length 20;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 20 RRCWGWYYY 11

RESULT 21
US-08-713-052-4
; Sequence 4, Application US/08713052
; Patent No. 5840673
; GENERAL INFORMATION:
; APPLICANT: Buckbinder, Leonard R.
; APPLICANT: Kley, Nikolai
; APPLICANT: Seizinger, Bernd
; TITLE OF INVENTION: Insulin-Like Growth Factor Binding
; TITLE OF INVENTION: Protein 3 (IGF-BP3) in Treatment of P53-Related Tumors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 12-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DC38a
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 252-5901
; TELEFAX: (609) 252-4526
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-713-052-4
  Query Match      100.0%; Score 10; DB 2; Length 21;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 21 RRCWGWYYY 12

REFERENCE/DOCKET NUMBER: DC38a
TELECOMMUNICATION INFORMATION:
  TELEPHONE: (609) 252-5901
  TELEFAX: (609) 252-4526
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
  LENGTH: 21 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: other nucleic acid
US-08-713-052-4
  Query Match      100.0%; Score 10; DB 2; Length 21;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 21 RRCWGWYYY 12

US-08-713-052-4/c
; Sequence 4, Application US/08713052
; Patent No. 5840673
; GENERAL INFORMATION:
; APPLICANT: Buckbinder, Leonard R.
; APPLICANT: Kley, Nikolai
; APPLICANT: Seizinger, Bernd
; TITLE OF INVENTION: Insulin-Like Growth Factor Binding
; TITLE OF INVENTION: Protein 3 (IGF-BP3) in Treatment of P53-Related Tumors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bristol-Myers Squibb Company
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 12-SEP-1996
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Gaul, Timothy J.
; REGISTRATION NUMBER: 33,111
; REFERENCE/DOCKET NUMBER: DC38a
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (609) 252-5901
; TELEFAX: (609) 252-4526
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 21 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-713-052-4
  Query Match      100.0%; Score 10; DB 2; Length 21;
  Best Local Similarity 100.0%; Pred. No. 0;
  Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 21 RRCWGWYYY 12
```

```
RESULT 23
US-08-446-668-8
; Sequence 8, Application US/08446668
; Patent No. 6140058
; GENERAL INFORMATION:
; APPLICANT: Lane, David P.
; ADDRESS: Flehr Hobbach Test Albritton & Herbert LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,668
; FILING DATE: 24-JUL-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61269/WH/MTK
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-446-668-8

Query Match          90.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWGY 9
Db 1 RRCWGWGY 9

RESULT 24
US-08-446-668-8/c
; Sequence 8, Application US/08446668
; Patent No. 6140058
; GENERAL INFORMATION:
; APPLICANT: Lane, David P.
; ADDRESS: Flehr Hobbach Test Albritton & Herbert LLP
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/446,668
; FILING DATE: 24-JUL-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-61269/WH/MTK
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-446-668-8

Query Match          90.0%; Score 9; DB 3; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCWGWYY 10
Db 9 RRCWGWYY 1

RESULT 25
US-09-196-099-15
; Sequence 15, Application US/09196099
; Patent No. 6465246
; GENERAL INFORMATION:
; APPLICANT: MUELLER, Rolf
; APPLICANT: SEDLACEK, Hans-Harald
; TITLE OF INVENTION: ONCOGENE- OR VIRUS-CONTROLLED EXPRESSION SYSTEM
; FILE REFERENCE: 26083/190
; CURRENT APPLICATION NUMBER: US/09/196,099
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: DE 19751587.8
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-196-099-15

Query Match          70.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWG 7
Db 1 RRCWGWG 7

RESULT 26
US-09-196-099-15/c
; Sequence 15, Application US/09196099
; Patent No. 6465246
; GENERAL INFORMATION:
; APPLICANT: MUELLER, Rolf
; APPLICANT: SEDLACEK, Hans-Harald
; TITLE OF INVENTION: ONCOGENE- OR VIRUS-CONTROLLED EXPRESSION SYSTEM
; FILE REFERENCE: 26083/190
; CURRENT APPLICATION NUMBER: US/09/196,099
; CURRENT FILING DATE: 1998-11-20
; EARLIER APPLICATION NUMBER: DE 19751587.8
; EARLIER FILING DATE: 1997-11-21
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn Ver. 2.0
```

; SEQ ID NO 15
; LENGTH: 7
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-196-099-15

Query Match 70.0%; Score 7; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWMGYYY 10
Db |||||
7 CWMGYYY 1

RESULT 27

US-08-299-074A-39
; Sequence 39, Application US/08299074A
; Patent No. 5955263
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; TITLE OF INVENTION: BY P53
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,074A
; FILING DATE: 01-SEP-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,758
; FILING DATE: 31-MAR-1992
; APPLICATION NUMBER: 07/715,182
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:

; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-299-074A-39

Query Match 50.0%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCW 5
Db |||||
1 RRCW 5

RESULT 28

US-08-299-074A-39/c
; Sequence 39, Application US/08299074A
; Patent No. 5955263
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; TITLE OF INVENTION: BY P53
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/299,074A
; FILING DATE: 01-SEP-1994
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,758
; FILING DATE: 31-MAR-1992
; APPLICATION NUMBER: 07/715,182
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:

; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-299-074A-39

Query Match 50.0%; Score 5; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WGYYY 10
Db |||||
5 WGYYY 1

RESULT 29

US-09-399-773-39
; Sequence 39, Application US/09399773
; Patent No. 6245515
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; TITLE OF INVENTION: BY P53
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA


```
;
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/399,773
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/299,074
; FILING DATE:
; APPLICATION NUMBER: 07/715,182
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-399-773-39

Query Match 50.0%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCW 5
Db 1 RRCW 5

RESULT 30
US-09-399-773-39/c
; Sequence 39, Application US/09399773
; Patent No. 6245515
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; TITLE OF INVENTION: BY P53
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/399,773
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/299,074
; FILING DATE:
; APPLICATION NUMBER: 07/715,182
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
```

```
;
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX:
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-09-399-773-39

Query Match 50.0%; Score 5; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGYYY 10
Db 5 WGYYY 1

RESULT 31
US-08-474-542A-134
; Sequence 134, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraime, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,542A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-542A-134

Query Match 50.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 WGGY 9
Db      11 WGGY 15

RESULT 32
US-08-474-542A-134/c
; Sequence 134, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Imprim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,542A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-474-542A-134

Query Match      50.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RRCW 6
Db      15 RRCW 11

RESULT 33
US-08-457-648-134
; Sequence 134, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Imprim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-457-648-134

Query Match      50.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WGGY 9
Db      11 WGGY 15

RESULT 34
US-08-457-648-134/c
; Sequence 134, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Imprim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 134:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-457-648-134

Query Match      50.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WGGY 9
Db      11 WGGY 15
```

ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-457-648-134

Query Match 50.0%; Score 5; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCWW 6
Db 15 RRCWW 11
|||||

RESULT 35
US-08-259-612A-9
Sequence 9, Application US/08259612A
Patent No. 5688918
GENERAL INFORMATION:
APPLICANT: Kulesz-Martin, Molly P.
TITLE OF INVENTION: p53as PROTEIN AND ANTIBODY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dunn & Associates, P.C.
STREET: P.O. Box 96
CITY: Newfane
STATE: New York
COUNTRY: U.S.A.
ZIP: 14108

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: Victor 300 SX/25 (IBM PC Compatible)
OPERATING SYSTEM: MS-DOS Version 5.0
SOFTWARE: Wordstar Professional Release 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,612A
FILING DATE: 14-Jun-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,952
FILING DATE: 14-Feb-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dunn, Michael L.
REGISTRATION NUMBER: 25,330
REFERENCE/DOCKET NUMBER: RPP:135B US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716) 433-1661
TELEFAX: (716) 433-1665
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 10
TYPE: Nucleic Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE:
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM:

STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: El - Diery et al.
TITLE: DEFINITION OF A CONGENOUS BINDING
TITLE: SITE FOR p53
JOURNAL: Nature Genetics
VOLUME: 1
ISSUE:
PAGES: 45-49
DATE: April, 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-259-612A-9

Query Match 40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWWG 7
Db 4 CWWG 7
|||||

RESULT 36
US-08-259-612A-9/c
Sequence 9, Application US/08259612A
Patent No. 5688918
GENERAL INFORMATION:
APPLICANT: Kulesz-Martin, Molly P.
TITLE OF INVENTION: p53as PROTEIN AND ANTIBODY
TITLE OF INVENTION: THEREFOR
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dunn & Associates, P.C.
STREET: P.O. Box 96
CITY: Newfane
STATE: New York
COUNTRY: U.S.A.
ZIP: 14108
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: Victor 300 SX/25 (IBM PC Compatible)
OPERATING SYSTEM: MS-DOS Version 5.0
SOFTWARE: Wordstar Professional Release 4
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/259,612A
FILING DATE: 14-Jun-1994
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,952
FILING DATE: 14-Feb-1994

ISSUE:
PAGES: 45-49
DATE: April, 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-644-291-9

Query Match 40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWG 7
| | | |
Db 4 CWG 7

RESULT 38
US-08-644-291-9/c
; Sequence 9, Application US/08644291
; Patent No. 5726024
; GENERAL INFORMATION:
; APPLICANT: Kulesz-Martin, Molly P.
; TITLE OF INVENTION: p53as PROTEIN AND ANTIBODY
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dunn & Associates
; STREET: P.O. Box 96
; CITY: Newfane
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 14108
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb
; MEDIUM TYPE: Storage
; COMPUTER: Victor 300 SX/25 (IBM PC Compatible)
; OPERATING SYSTEM: MS-DOS Version 5.0
; SOFTWARE: Wordstar Professional Release 4
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/644,291
; FILING DATE: 10-May-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/259,612
; FILING DATE: 14-Jun-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/195,952
; FILING DATE: 11-Feb-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/100,496
; FILING DATE: 02-Aug-1993
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Dunn, Michael L.
; REGISTRATION NUMBER: 25,330
; REFERENCE/POCKET NUMBER: RPP:135E US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (716) 433-1661
; TELEFAX: (716) 433-1665
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10
; TYPE: Nucleic Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE:
; HYPOTHETICAL: No
; ANTI-SENSE: No
; FRAGMENT TYPE:

ORIGINAL SOURCE:
ORGANISM:
STRAIN:
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE:
HAPLOTYPE:
TISSUE TYPE:
CELL TYPE:
CELL LINE:
ORGANELLE:
IMMEDIATE SOURCE:
LIBRARY:
CLONE:
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
MAP POSITION:
UNITS:
FEATURE:
NAME/KEY:
LOCATION:
IDENTIFICATION METHOD:
OTHER INFORMATION:
PUBLICATION INFORMATION:
AUTHORS: El - Diery et al.
TITLE: DEFINITION OF A CONCENCUS BINDING
TITLE: SITE FOR p53
JOURNAL: Nature Genetics
VOLUME: 1
ISSUE:
PAGES: 45-49
DATE: April, 1992
DOCUMENT NUMBER:
FILING DATE:
PUBLICATION DATE:
RELEVANT RESIDUES IN SEQ ID NO:
US-08-644-291-9

Query Match 40.0%; Score 4; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWG 7
| | | |
Db 7 CWG 4

RESULT 39
US-09-672-717-212
; Sequence 212, Application US/09672717
; Patent No. 6673917
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Lacasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; TITLE OF INVENTION: Thereof
; FILE REFERENCE: 07891/025001
; CURRENT APPLICATION NUMBER: US/09/672,717
; CURRENT FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1,17,18
; OTHER INFORMATION: y=um
; NAME/KEY: modified_base
; LOCATION: 19


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-474-542A-133

Query Match          40.0%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      3 RCW 6
      ||||
Db      14 RCW 11

RESULT 43
US-08-474-542A-135
; Sequence 135, Application US/08474542A
; Patent No. 5527898
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraime, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,542A
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9234
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-474-542A-135

Query Match          40.0%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 RCW 5
      ||||
Db      15 RCW 12

RESULT 45
US-08-457-648-133
; Sequence 133, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Impraime, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
```

COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,648
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-457-648-133

Query Match 40.0%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WGY 8
DB 11 WGY 14

RESULT 46
US-08-457-648-133/c
Sequence 133, Application US/08457648
Patent No. 5639871
GENERAL INFORMATION:
APPLICANT: Bauer, Heidi M.
APPLICANT: Gravitt, Patti E.
APPLICANT: Greer, Catherine E.
APPLICANT: Impra, Chaka C.
APPLICANT: Manos, M. Michele
APPLICANT: Resnick, Robert M.
TITLE OF INVENTION: Detection of Human Papillomavirus by the
NUMBER OF SEQUENCES: 298
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,648
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977

INFORMATION FOR SEQ ID NO: 133:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-457-648-133

Query Match 40.0%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RCW 6
DB 14 RCW 11

RESULT 47
US-08-457-648-135
Sequence 135, Application US/08457648
Patent No. 5639871
GENERAL INFORMATION:
APPLICANT: Bauer, Heidi M.
APPLICANT: Gravitt, Patti E.
APPLICANT: Greer, Catherine E.
APPLICANT: Impra, Chaka C.
APPLICANT: Manos, M. Michele
APPLICANT: Resnick, Robert M.
TITLE OF INVENTION: Detection of Human Papillomavirus by the
NUMBER OF SEQUENCES: 298
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457,648
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Petry, Douglas A.
REGISTRATION NUMBER: 35,321
REFERENCE/DOCKET NUMBER: 9205
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 814-2974
TELEFAX: (510) 814-2977
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-457-648-135

Query Match 40.0%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WGY 9
DB 12 WGY 15

RESULT 48
US-08-457-648-135/c
; Sequence 135, Application US/08457648
; Patent No. 5639871
; GENERAL INFORMATION:
; APPLICANT: Bauer, Heidi M.
; APPLICANT: Gravitt, Patti E.
; APPLICANT: Greer, Catherine E.
; APPLICANT: Imprim, Chaka C.
; APPLICANT: Manos, M. Michele
; APPLICANT: Resnick, Robert M.
; TITLE OF INVENTION: Detection of Human Papillomavirus by the
; TITLE OF INVENTION: Polymerase Chain Reaction
; NUMBER OF SEQUENCES: 298
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,648
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Petry, Douglas A.
; REGISTRATION NUMBER: 35,321
; REFERENCE/DOCKET NUMBER: 9205
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (510) 814-2974
; TELEFAX: (510) 814-2977
; INFORMATION FOR SEQ ID NO: 135:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-457-648-135

Query Match 40.0%; Score 4; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCW 5
Db 15 RRCW 12

RESULT 49
US-08-657-828A-3
; Sequence 3, Application US/08657828A
; Patent No. 5876711
; GENERAL INFORMATION:
; APPLICANT: Fattaey, Ali
; TITLE OF INVENTION: Methods and Compositions for Determining
; TITLE OF INVENTION: the Tumor Suppressor Status of Cells
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Onyx Pharmaceuticals, Inc.
; STREET: 3031 Research Drive
; CITY: Richmond
; STATE: CA
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,828A
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Giotta, Gregory
; REGISTRATION NUMBER: 32,028
; REFERENCE/DOCKET NUMBER: ONYX1021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-262-8710
; TELEFAX: 510-758-3405
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-657-828A-3

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCR 4
Db 1 RRCR 4

RESULT 50
US-08-657-828A-3/c
; Sequence 3, Application US/08657828A
; Patent No. 5876711
; GENERAL INFORMATION:
; APPLICANT: Fattaey, Ali
; TITLE OF INVENTION: Methods and Compositions for Determining
; TITLE OF INVENTION: the Tumor Suppressor Status of Cells
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Onyx Pharmaceuticals, Inc.
; STREET: 3031 Research Drive
; CITY: Richmond
; STATE: CA
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/657,828A
; FILING DATE: 31-MAY-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Giotta, Gregory
; REGISTRATION NUMBER: 32,028
; REFERENCE/DOCKET NUMBER: ONYX1021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-262-8710
; TELEFAX: 510-758-3405
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

```

; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-657-828A-3

Query Match 40.0%; Score 4; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRC 4
Db 20 RRC 17

RESULT 51
US-09-260-420-3
; Sequence 3, Application US/09260420
; Patent No. 6391630
; GENERAL INFORMATION:
; APPLICANT: Fattaey, Ali
; TITLE OF INVENTION: Methods and Compositions for Determining
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Onyx Pharmaceuticals, Inc.
; STREET: 3031 Research Drive
; CITY: Richmond
; STATE: CA
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/260,420
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/657,828
; FILING DATE: 31-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Giotta, Gregory
; REGISTRATION NUMBER: 32,028
; REFERENCE/DOCKET NUMBER: ONYX1021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-262-8710
; TELEFAX: 510-758-3405
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-260-420-3

Query Match 40.0%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRC 4
Db 20 RRC 17

RESULT 52
US-09-260-420-3/c
; Sequence 3, Application US/09260420
; Patent No. 6391630
; GENERAL INFORMATION:
; APPLICANT: Fattaey, Ali
; TITLE OF INVENTION: Methods and Compositions for Determining
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Onyx Pharmaceuticals, Inc.
; STREET: 3031 Research Drive
; CITY: Richmond
; STATE: CA
; COUNTRY: USA
; ZIP: 94806
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/260,420
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/657,828
; FILING DATE: 31-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Giotta, Gregory
; REGISTRATION NUMBER: 32,028
; REFERENCE/DOCKET NUMBER: ONYX1021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 510-262-8710
; TELEFAX: 510-758-3405
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-09-260-420-3

Query Match 40.0%; Score 4; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRC 4
Db 20 RRC 17

RESULT 53
US-07-959-119A-8
; Sequence 8, Application US/07959119A
; Patent No. 5487985
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

```

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/07/959,119A
;; FILING DATE: 09-OCT-1992
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Halluin, Albert P.
;; REGISTRATION NUMBER: 25,227
;; REFERENCE/DOCKET NUMBER: 8142-021
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 854-3660
;; TELEFAX: (415) 854-3694
;; TELEX: 66141PENNIE
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 27 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: DNA (genomic)
US-07-959-119A-8

Query Match 40.0%; Score 4; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4
DB 15 RRCR 18

RESULT 54
US-07-959-119A-8/c
; Sequence 8, Application US/07959119A
; Patent No. 5487985
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,119A
FILING DATE: 09-OCT-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8142-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-07-959-119A-8
Query Match 40.0%; Score 4; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4
DB 15 RRCR 18

RESULT 56
US-07-959-119A-9/c
; Sequence 9, Application US/07959119A
; Patent No. 5487985
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes

Query Match 40.0%; Score 4; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10
DB 18 GYYY 15

RESULT 55
US-07-959-119A-9
; Sequence 9, Application US/07959119A
; Patent No. 5487985
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,119A
FILING DATE: 09-OCT-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8142-021
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 854-3660
TELEFAX: (415) 854-3694
TELEX: 66141PENNIE
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)

US-07-959-119A-9
Query Match 40.0%; Score 4; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4
DB 15 RRCR 18

RESULT 56
US-07-959-119A-9/c
; Sequence 9, Application US/07959119A
; Patent No. 5487985
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes

/ NUMBER OF SEQUENCES: 16
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 2730 Sand Hill Road
/ CITY: Menlo Park
/ STATE: California
/ COUNTRY: U.S.A.
/ ZIP: 94025
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/959,119A
/ FILING DATE: 09-OCT-1992
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Halluin, Albert P.
/ REGISTRATION NUMBER: 25,227
/ REFERENCE/DOCKET NUMBER: 8142-021
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 854-3660
/ TELEFAX: (415) 854-3694
/ TELEX: 66141PENNIE
/ INFORMATION FOR SEQ ID NO: 9:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 27 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ US-07-959-119A-9

Query Match 40.0%; Score 4; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10
Db 18 GYYY 15

RESULT 57
US-08-471-994-7
/ Sequence 7, Application US/08471994
/ Patent No. 5861245
/ GENERAL INFORMATION:
/ APPLICANT: McClelland, Michael
/ APPLICANT: Welsh, John T.
/ APPLICANT: Sorge, Joseph A.
/ TITLE OF INVENTION: ARBITRARILY PRIMED POLYMERASE CHAIN
/ TITLE OF INVENTION: REACTION METHOD FOR FINGERPRINTING GENOMES
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States of America
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/471,994
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Halluin, Albert P.
/ REGISTRATION NUMBER: 25,227

/ REFERENCE/DOCKET NUMBER: 8142-103
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-854-3660
/ TELEFAX: 415-854-3694
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 27 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ US-08-471-994-7

Query Match 40.0%; Score 4; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRR 4
Db 15 RRRR 18

RESULT 58
US-08-471-994-7/C
/ Sequence 7, Application US/08471994
/ Patent No. 5861245
/ GENERAL INFORMATION:
/ APPLICANT: McClelland, Michael
/ APPLICANT: Welsh, John T.
/ APPLICANT: Sorge, Joseph A.
/ TITLE OF INVENTION: ARBITRARILY PRIMED POLYMERASE CHAIN
/ TITLE OF INVENTION: REACTION METHOD FOR FINGERPRINTING GENOMES
/ NUMBER OF SEQUENCES: 13
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Pennie & Edmonds
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States of America
/ ZIP: 10036
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/471,994
/ FILING DATE: 06-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Halluin, Albert P.
/ REGISTRATION NUMBER: 25,227
/ REFERENCE/DOCKET NUMBER: 8142-103
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-854-3660
/ TELEFAX: 415-854-3694
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 7:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 27 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: unknown
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ US-08-471-994-7

Query Match 40.0%; Score 4; DB 2; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10
Db 18 GYYY 15

Db 18 GYYY 15

RESULT 59
US-08-471-994-11
; Sequence 11, Application US/08471994
; Patent No. 5861245
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: ARBITRARILY PRIMED POLYMERASE CHAIN
; TITLE OF INVENTION: REACTION METHOD FOR FINGERPRINTING GENOMES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,994
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8142-103
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-471-994-11

Query Match 40.0%; Score 4; DB 2; Length 27;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRR 4
|||
Db 15 RRRR 18

RESULT 60
US-08-471-994-11/c
; Sequence 11, Application US/08471994
; Patent No. 5861245
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: ARBITRARILY PRIMED POLYMERASE CHAIN
; TITLE OF INVENTION: REACTION METHOD FOR FINGERPRINTING GENOMES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America

ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,994
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8142-103
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: DNA (genomic)
US-08-471-994-11

Query Match 40.0%; Score 4; DB 2; Length 27;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10
|||
Db 18 GYYY 15

RESULT 61
US-08-154-364-7
; Sequence 7, Application US/08154364
; Patent No. 6207810
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: ARBITRARILY PRIMED
; TITLE OF INVENTION: POLYMERASE CHAIN
; TITLE OF INVENTION: REACTION METHOD FOR FINGER PRINTING
; TITLE OF INVENTION: GENOMES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach and Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/154,364
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bortner, Scott R.
REGISTRATION NUMBER: 34,298
REFERENCE/DOCKET NUMBER: STRG-20142 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 414-433-8716

; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-154-364-7

Query Match 40.0%; Score 4; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4
DB 15 RRCR 18

RESULT 62
US-08-154-364-7/c
; Sequence 7, Application US/08154364
; Patent No. 6207810
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; TITLE OF INVENTION: ARBITRARILY PRIMED
; TITLE OF INVENTION: POLYMERASE CHAIN
; TITLE OF INVENTION: REACTION METHOD FOR FINGER PRINTING
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Limbach and Limbach
; STREET: 2001 Ferry Building
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111

COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
APPLICATION NUMBER: US/08/154,364

CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Borthner, Scott R.
REGISTRATION NUMBER: 34,298
REFERENCE/DOCKET NUMBER: STRG-20142 USA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-433-4150
TELEFAX: 414-433-8716
INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-154-364-7

Query Match 40.0%; Score 4; DB 3; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYYY 10

DB 18 GYYY 15

RESULT 63
US-08-397-335-8
; Sequence 8, Application US/08397335
; Patent No. 6696277
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,335
; FILING DATE: Concurrently herewith.
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,119
; FILING DATE: 09-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-397-335-8

Query Match 40.0%; Score 4; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCR 4
DB 15 RRCR 18

RESULT 64
US-08-397-335-8/c
; Sequence 8, Application US/08397335
; Patent No. 6696277
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

```

; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,335
; FILING DATE: Concurrently herewith.
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,119
; FILING DATE: 09-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-397-335-8

Query Match 40.0%; Score 4; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
Db 18 GYYY 15

RESULT 65
US-08-397-335-9
; Sequence 9, Application US/08397335
; Patent No. 6696277
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,335
; FILING DATE: Concurrently herewith.
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,119
; FILING DATE: 09-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-397-335-9
```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-397-335-9

Query Match 40.0%; Score 4; DB 4; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
Db 15 RRRC 18

RESULT 66
US-08-397-335-9/c
; Sequence 9, Application US/08397335
; Patent No. 6696277
; GENERAL INFORMATION:
; APPLICANT: McClelland, Michael
; APPLICANT: Welsh, John T.
; APPLICANT: Sorge, Joseph A.
; TITLE OF INVENTION: Arbitrarily Primed Polymerase Chain
; TITLE OF INVENTION: Reaction Method For Fingerprinting Genomes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 2730 Sand Hill Road
; CITY: Menlo Park
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94025
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/397,335
; FILING DATE: Concurrently herewith.
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,119
; FILING DATE: 09-DEC-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 8142-092
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-3660
; TELEFAX: (415) 854-3694
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 27 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-397-335-9
```

Query Match 40.0%; Score 4; DB 4; Length 27;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYY 10
Db 18 GYY 15

RESULT 67
US-09-347-343-1
; Sequence 1, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-1

Query Match 30.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
Db 1 RRC 3

RESULT 68
US-09-347-343-1/c
; Sequence 1, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-1

Query Match 30.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
Db 6 RRC 4

RESULT 69
US-09-347-343-2
; Sequence 2, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE

; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-2

Query Match 30.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYY 9
Db 4 GYY 6

RESULT 70
US-09-347-343-2/c
; Sequence 2, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-2

Query Match 30.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
Db 6 RRC 4

RESULT 71
US-09-936-552A-4
; Sequence 4, Application US/09936552A
; Patent No. 6610907
; GENERAL INFORMATION:
; APPLICANT: INSTITUTE OF GENETICS, CHINESE ACADEMY OF SCIENCES
; APPLICANT: Zhu, Zhen
; APPLICANT: Xie, Yinggu
; APPLICANT: Liu, Yule
; TITLE OF INVENTION: COTTON LEAF CURL VIRUS (CLCV) PROMOTER AND ITS USE
; FILE REFERENCE: 2896-4001
; CURRENT APPLICATION NUMBER: US/09/936,552A
; CURRENT FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: CN 99103044.3
; PRIOR FILING DATE: 1999-03-22
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Cotton leaf curl virus

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(3)
; OTHER INFORMATION: y=pyrimidine

; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (5)_(5)
; OTHER INFORMATION: y-pyrimidine
US-09-936-552A-4

Query Match 30.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
|||
Db 1 YYY 3

RESULT 72
US-09-936-552A-4/c
; Sequence 4, Application US/09936552A
; Patent No. 6610907
; GENERAL INFORMATION:

; APPLICANT: INSTITUTE OF GENETICS, CHINESE ACADEMY OF SCIENCES
; APPLICANT: Zhu, Zhen

; APPLICANT: Xie, Yingqiu

; APPLICANT: Liu, Yule

; TITLE OF INVENTION: COTTON LEAF CURL VIRUS (CLCUV) PROMOTER AND ITS USE
; FILE REFERENCE: 2896-4001

; CURRENT APPLICATION NUMBER: US/09/936,552A

; CURRENT FILING DATE: 2001-09-14

; PRIOR APPLICATION NUMBER: CN 99103044.3

; PRIOR FILING DATE: 1999-03-22

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 4

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Cotton leaf curl virus

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (1)_(3)

; OTHER INFORMATION: y-pyrimidine

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: (5)_(5)

; OTHER INFORMATION: y-pyrimidine
US-09-936-552A-4

Query Match 30.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
|||
Db 3 RRR 1

RESULT 73
US-09-936-552A-8
; Sequence 8, Application US/09263692A
; Patent No. 6639065
; GENERAL INFORMATION:

; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A chemically synthesized artificial promoter for high level expression

; FILE REFERENCE: Q52511
; CURRENT APPLICATION NUMBER: US/09/263,692A

; CURRENT FILING DATE: 1999-03-05

; PRIOR APPLICATION NUMBER: 3322/Del/98

; PRIOR FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: domain II(b)
US-09-263-692A-8

Query Match 30.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWW 6
|||
Db 1 CWW 3

RESULT 74
US-09-263-692A-8/c
; Sequence 8, Application US/09263692A
; Patent No. 6639065
; GENERAL INFORMATION:

; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A chemically synthesized artificial promoter for high level expression

; FILE REFERENCE: Q52511
; CURRENT APPLICATION NUMBER: US/09/263,692A

; CURRENT FILING DATE: 1999-03-05

; PRIOR APPLICATION NUMBER: 3322/Del/98

; PRIOR FILING DATE: 1998-11-09

; NUMBER OF SEQ ID NOS: 20

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 8

; LENGTH: 6

; TYPE: DNA

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: domain II(b)
US-09-263-692A-8

Query Match 30.0%; Score 3; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7
|||
Db 6 WWG 4

RESULT 75
US-08-646-301A-9
; Sequence 9, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
; TITLE OF INVENTION: Antigen for Expression Targeting

; FILE REFERENCE: PB1508USW

; CURRENT APPLICATION NUMBER: US/08/646,301A

; CURRENT FILING DATE: 1996-05-16

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 8

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: consensus

; OTHER INFORMATION: sequence B2 from DNA Sequence 1:3-11 (1990).

; Patent No. 6194211
US-08-646-301A-9

Query Match 30.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7
|||
Db 6 WWG 8

RESULT 76

US-08-646-301A-9/c
; Sequence 9, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
; Patent No. 6194211
; TITLE OF INVENTION: Antigen for Expression Targeting
; FILE REFERENCE: FB1508USW
; CURRENT APPLICATION NUMBER: US/08/646,301A
; CURRENT FILING DATE: 1996-05-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; Patent No. 6194211
US-08-646-301A-9

Query Match 30.0%; Score 3; DB 3; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWW 6
|||
Db 8 CWW 6

RESULT 77

US-09-305-839-41
; Sequence 41, Application US/09305839
; Patent No. 6514935
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; TITLE OF INVENTION: Methods of Treating Hypertension
; FILE REFERENCE: 21508-064
; CURRENT APPLICATION NUMBER: US/09/305,839
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 08/818,655
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-305-839-41

Query Match 30.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
|||
Db 6 YYY 8

RESULT 78

US-09-305-839-41/c
; Sequence 41, Application US/09305839
; Patent No. 6514935
; GENERAL INFORMATION:
; APPLICANT: Lee, Mu-En
; TITLE OF INVENTION: Methods of Treating Hypertension
; FILE REFERENCE: 21508-064
; CURRENT APPLICATION NUMBER: US/09/305,839
; CURRENT FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: 08/818,655
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 41
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
US-09-305-839-41

Query Match 30.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
|||
Db 8 RRR 6

RESULT 79

US-09-347-343-3
; Sequence 3, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-3

Query Match 30.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
|||
Db 1 RRC 3

RESULT 80

US-09-347-343-3/c
; Sequence 3, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01

; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-3

Query Match 30.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 6 RRC 4

RESULT 81
US-09-347-343-4
; Sequence 4, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-4

Query Match 30.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9
|||
Db 4 GY 6

RESULT 82
US-09-347-343-4/c
; Sequence 4, Application US/09347343A
; Patent No. 6514948
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/09/347,343A
; CURRENT FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-09-347-343-4

Query Match 30.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 6 RRC 4

RESULT 83
US-09-263-692A-7
; Sequence 7, Application US/09263692A
; Patent No. 6639065
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A chemically synthesized artificial promoter for high level expression of transgenes and a method for its synthesis
; FILE REFERENCE: Q52511
; CURRENT APPLICATION NUMBER: US/09/263,692A
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: 3322/Del/98
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: domain II(a)
US-09-263-692A-7

Query Match 30.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 1 RRR 3

RESULT 84
US-09-263-692A-7/c
; Sequence 7, Application US/09263692A
; Patent No. 6639065
; GENERAL INFORMATION:
; APPLICANT: Council of Scientific and Industrial Research
; TITLE OF INVENTION: A chemically synthesized artificial promoter for high level expression of transgenes and a method for its synthesis
; FILE REFERENCE: Q52511
; CURRENT APPLICATION NUMBER: US/09/263,692A
; CURRENT FILING DATE: 1999-03-05
; PRIOR APPLICATION NUMBER: 3322/Del/98
; PRIOR FILING DATE: 1998-11-09
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: domain II(a)
US-09-263-692A-7

Query Match 30.0%; Score 3; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 8 YYY 6

RESULT 85
US-07-882-838E-1
; Sequence 1, Application US/07882838E
; Patent No. 5616461
; GENERAL INFORMATION:
; APPLICANT: Priscilla A. Schaffer
; APPLICANT: Christine E. Dabrowski Amara1

;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
;; TITLE OF INVENTION: TREATMENT OF VIRUS INFECTIONS
;; NUMBER OF SEQUENCES: 49
;; CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn
STREET: One Liberty Place
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/882,838E

FILING DATE: May 14, 1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kathryn Leary

REGISTRATION NUMBER: 36,317

REFERENCE/DOCKET NUMBER: DFCI-0001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-07-882-838E-1

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10

Db 4 YYY 6

RESULT 86

US-07-882-838E-1/c

Sequence 1, Application US/07882838E

Patent No. 5616461

GENERAL INFORMATION:

APPLICANT: Priscilla A. Schaffer

APPLICANT: Christine E. Dabrowski Amara

TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR

TITLE OF INVENTION: TREATMENT OF VIRUS INFECTIONS

NUMBER OF SEQUENCES: 49

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock Washburn

STREET: One Liberty Place

CITY: Philadelphia

STATE: Pennsylvania

COUNTRY: U.S.A.

ZIP: 19103

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/07/882,838E

FILING DATE: May 14, 1992

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER:

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Kathryn Leary

REGISTRATION NUMBER: 36,317

REFERENCE/DOCKET NUMBER: DFCI-0001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (215) 568-3100

TELEFAX: (215) 568-3439

TELEX:

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 9

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-07-882-838E-1

Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3

Db 6 RRR 4

RESULT 87

US-08-643-886-11

Sequence 11, Application US/08643886

Patent No. 5695977

GENERAL INFORMATION:

APPLICANT: JURKA, Jerzy W.

TITLE OF INVENTION: Site Directed Recombination

NUMBER OF SEQUENCES: 22

CORRESPONDENCE ADDRESS:

ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: CA

COUNTRY: US

ZIP: 94111

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/643,886

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I

REGISTRATION NUMBER: 20015

REFERENCE/DOCKET NUMBER: A-63252/BI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-781-1989

TELEFAX: 415-398-3249

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "sequence"

US-08-643-886-11

Query Match

Best Local Similarity 30.0%; Score 3; DB 1; Length 9;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 6 RRR 8

RESULT 88
US-08-643-886-11/c
; Sequence 11, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"

US-08-643-886-11
Query Match 30.0%; Score 3; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 YYY 10
Db 8 YYY 6

RESULT 89
US-08-122-433-34
; Sequence 34, Application US/08122433
; Patent No. 5683985
; GENERAL INFORMATION:
; APPLICANT: Chu, Barbara C.F.
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND
; ADDRESSEE: Orgel, Leslie
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/122,433
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/687,337
; FILING DATE: 18-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 9308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-1995
; TELEFAX: 619-546-9392
; INFORMATION FOR SEQ ID NO: 34:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
US-08-122-433-34

Query Match 30.0%; Score 3; DB 1; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 4 CWW 6
Db 2 CWW 4

RESULT 90
US-08-122-433-34/c
; Sequence 34, Application US/08122433
; Patent No. 5683985
; GENERAL INFORMATION:
; APPLICANT: Chu, Barbara C.F.
; TITLE OF INVENTION: OLIGODEOXYNUCLEOTIDES AND
; ADDRESSEE: Orgel, Leslie
; STREET: 444 South Flower Street, Suite 2000
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/122,433
; FILING DATE: 22-SEP-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/687,337
; FILING DATE: 18-APR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Reiter, Stephen E.
; REGISTRATION NUMBER: 31,192
; REFERENCE/DOCKET NUMBER: P31 9308
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619-546-1995

TELEFAX: 619-546-9392
 INFORMATION FOR SEQ ID NO: 34:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 US-08-122-433-34

Query Match 30.0%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
 Db 9 CWW 7

RESULT 91
 US-08-643-886-1
 ; Sequence 1, Application US/08643886
 ; Patent No. 5695977
 ; GENERAL INFORMATION:
 ; APPLICANT: JURKA, Jerzy W.
 ; TITLE OF INVENTION: Site Directed Recombination
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/643,886
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: A-63252/BIR
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "sequence"

Query Match 30.0%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
 Db 7 YYY 9

RESULT 92
 US-08-643-886-1/c
 ; Sequence 1, Application US/08643886
 ; Patent No. 5695977

GENERAL INFORMATION:
 APPLICANT: JURKA, Jerzy W.
 TITLE OF INVENTION: Site Directed Recombination
 NUMBER OF SEQUENCES: 22
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 STREET: Four Embarcadero Center, Suite 3400
 CITY: San Francisco
 STATE: CA
 COUNTRY: US
 ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/643,886
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I
 REGISTRATION NUMBER: 20015
 REFERENCE/DOCKET NUMBER: A-63252/BIR
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-781-1989
 TELEFAX: 415-398-3249
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 DESCRIPTION: /desc = "sequence"

Query Match 30.0%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
 Db 9 RRR 7

RESULT 93
 US-08-643-886-12
 ; Sequence 12, Application US/08643886
 ; Patent No. 5695977
 ; GENERAL INFORMATION:
 ; APPLICANT: JURKA, Jerzy W.
 ; TITLE OF INVENTION: Site Directed Recombination
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/643,886
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Rowland, Bertram I
 REGISTRATION NUMBER: 20015

Query Match 30.0%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
 Db 7 YYY 9

RESULT 92
 US-08-643-886-1/c
 ; Sequence 1, Application US/08643886
 ; Patent No. 5695977

; REFERENCE/DOCKET NUMBER: A-63252/BIR
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "sequence"
 ; US-08-643-886-12

Query Match 30.0%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
 |||
 Db 7 RRR 9

RESULT 94
 US-08-643-886-12/c
 ; Sequence 12, Application US/08643886
 ; Patent No. 5695977
 ; GENERAL INFORMATION:
 ; APPLICANT: JURKA, Jerzy W.
 ; TITLE OF INVENTION: Site Directed Recombination
 ; NUMBER OF SEQUENCES: 22
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
 ; STREET: Four Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: US
 ; ZIP: 94111
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/643,886
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Rowland, Bertram I
 ; REGISTRATION NUMBER: 20015
 ; REFERENCE/DOCKET NUMBER: A-63252/BIR
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-781-1989
 ; TELEFAX: 415-398-3249
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: other nucleic acid
 ; DESCRIPTION: /desc = "sequence"
 ; US-08-643-886-12

Query Match 30.0%; Score 3; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
 |||
 Db 9 YYY 7

RESULT 95
 US-08-472-809B-5
 ; Sequence 5, Application US/08472809B
 ; Patent No. 5925564
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwartz, Robert J.
 ; APPLICANT: DeMayo, Franco J.
 ; APPLICANT: O'Malley, Bert W.
 ; TITLE OF INVENTION: Expression Vector Systems and
 ; METHOD OF INVENTION: Method of Use
 ; NUMBER OF SEQUENCES: 8
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Lyon & Lyon
 ; STREET: 633 West Fifth Street
 ; CITY: Los Angeles
 ; STATE: California
 ; COUNTRY: U.S.A.
 ; ZIP: 90071-2066
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ; MEDIUM TYPE: storage
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: IBM P.C. DOS 5.0
 ; SOFTWARE: Word Perfect 5.1
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/472,809B
 ; FILING DATE: June 7, 1995
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/209,846
 ; FILING DATE: March 9, 1994
 ; APPLICATION NUMBER: 07/789,919
 ; FILING DATE: No. 5925564member 6, 1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Warburg, Richard J.
 ; REGISTRATION NUMBER: 32,327
 ; REFERENCE/DOCKET NUMBER: 214/212
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (213) 489-1600
 ; TELEFAX: (213) 955-0440
 ; TELEX: 67-3510
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 10 bases
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cdna
 ; FEATURE:
 ; OTHER INFORMATION: /note= W = A or T
 ; US-08-472-809B-5

Query Match 30.0%; Score 3; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
 |||
 Db 2 CWW 4

RESULT 96
 US-08-472-809B-5/c
 ; Sequence 5, Application US/08472809B
 ; Patent No. 5925564
 ; GENERAL INFORMATION:
 ; APPLICANT: Schwartz, Robert J.
 ; APPLICANT: DeMayo, Franco J.
 ; APPLICANT: O'Malley, Bert W.
 ; TITLE OF INVENTION: Expression Vector Systems and
 ; METHOD OF INVENTION: Method of Use
 ; NUMBER OF SEQUENCES: 8

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Initiator consensus sequence
US-08-481-658B-23

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 10 RRR 8

RESULT 99
US-08-477-504A-23
Sequence 23, Application US/08477504A
Patent No. 5972353

GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Initiator consensus sequence
US-08-477-504A-23

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 100
US-08-477-504A-23/c
Sequence 23, Application US/08477504A

Patent No. 5972353
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994

ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Initiator consensus sequence
US-08-477-504A-23

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 10 RRR 8

RESULT 101
US-08-486-756A-23
Sequence 23, Application US/08486756A
Patent No. 5981711

GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

;
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
; US-08-486-756A-23

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
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Db 1 YYY 3

RESULT 102
US-08-486-756A-23/c
; Sequence 23, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3C
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs

;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
; US-08-486-756A-23

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
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Db 10 RRR 8

RESULT 103
US-08-485-862B-23
; Sequence 23, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,862B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
; US-08-485-862B-23

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
|||
Db 1 YYY 3

RESULT 104

US-08-485-862B-23/c
; Sequence 23, Application US/08485862B
; Patent No. 5989838
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street, Suite 610
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485.862B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
US-08-485-862B-23

Query Match 30.0%; Score 3; DB 2; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 10 RRR 8

RESULT 105

US-08-787-739-23
; Sequence 23, Application US/08787739
; Patent No. 6027887
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street, Suite 610
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104

ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/787,739
; FILING DATE: 24-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/486,756
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/477,504
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/481,658
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,862
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/485,863
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/487,077
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
US-08-787-739-23

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 106

US-08-787-739-23/c
; Sequence 23, Application US/08787739
; Patent No. 6027887
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 96
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street, Suite 610
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104

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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION NUMBER: US/08/787,739
FILING DATE: 24-JAN-1997
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: US 08/485,049
  FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: US 08/486,756
  FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: US 08/477,504
  FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: US 08/481,658
  FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: US 08/485,862
  FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: US 08/485,863
  FILING DATE: 07-JUN-1995
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: US 08/487,077
  FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
  NAME: Lauder, Leona L.
  REGISTRATION NUMBER: 30,863
  REFERENCE/DOCKET NUMBER: D-0021.4
  TELEPHONE: 415-981-2034
  TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
  LENGTH: 10 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Initiator consensus sequence
US-08-787-739-23

Query Match          30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 10 RRR 8

RESULT 107
US-08-742-877-13
Sequence 13, Application US/08742877
Patent No. 6046380
GENERAL INFORMATION:
  APPLICANT: CLARK, Anthony J.
  TITLE OF INVENTION: DNA SEQUENCES
  NUMBER OF SEQUENCES: 14
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
  STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
  CITY: WASHINGTON
  STATE: DC
  COUNTRY: USA
  ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/742,877
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: GB 9408717.8
  FILING DATE: 03-MAY-1994
  NAME: FLESHNER, RAZ E.
  REGISTRATION NUMBER: 34,331
  REFERENCE/DOCKET NUMBER: 0623.0470001/REF
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 371-2600
  TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
  LENGTH: 10 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  MEDIUM TYPE: Floppy disk
  COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/742,877
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: GB 9408717.8
  FILING DATE: 03-MAY-1994
  NAME: FLESHNER, RAZ E.
  REGISTRATION NUMBER: 34,331
  REFERENCE/DOCKET NUMBER: 0623.0470001/REF
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 371-2600
  TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
  LENGTH: 10 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: mRNA
US-08-742-877-13

Query Match          30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 108
US-08-742-877-13/c
Sequence 13, Application US/08742877
Patent No. 6046380
GENERAL INFORMATION:
  APPLICANT: CLARK, Anthony J.
  TITLE OF INVENTION: DNA SEQUENCES
  NUMBER OF SEQUENCES: 14
  CORRESPONDENCE ADDRESS:
  ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX, P.L.L.C.
  STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
  CITY: WASHINGTON
  STATE: DC
  COUNTRY: USA
  ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/742,877
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
  APPLICATION NUMBER: GB 9408717.8
  FILING DATE: 03-MAY-1994
  NAME: FLESHNER, RAZ E.
  REGISTRATION NUMBER: 34,331
  REFERENCE/DOCKET NUMBER: 0623.0470001/REF
  TELECOMMUNICATION INFORMATION:
  TELEPHONE: (202) 371-2600
  TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
  LENGTH: 10 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: mRNA
US-08-742-877-13

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 6 RRR 4

RESULT 109

US-08-487-077A-23

; Sequence 23, Application US/08487077A

; Patent No. 6069242

; GENERAL INFORMATION:

; APPLICANT: Zavada, Jan

; APPLICANT: Pastorekova, Silvia

; APPLICANT: Pastorek, Jaromir

; TITLE OF INVENTION: MN Gene and Protein

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leona L. Lauder

; STREET: 6 Mariposa Court

; CITY: Tiburon

; STATE: California

; COUNTRY: USA

; ZIP: 94920

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,077A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/260,190

; FILING DATE: 15-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863

; REFERENCE/DOCKET NUMBER: D-0021.3H

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-435-2034

; TELEFAX: 415-435-0727

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; DESCRIPTION: Initiator consensus sequence

US-08-487-077A-23

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 110

US-08-487-077A-23/C

; Sequence 23, Application US/08487077A

; Patent No. 6069242

; GENERAL INFORMATION:

; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/487,077A

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/260,190

; FILING DATE: 15-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863

; REFERENCE/DOCKET NUMBER: D-0021.3H

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-435-2034

; TELEFAX: 415-435-0727

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; DESCRIPTION: Initiator consensus sequence

US-08-487-077A-23

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 10 RRR 8

RESULT 111

US-08-726-807B-47

; Sequence 47, Application US/08726807B

; Patent No. 6090618

; GENERAL INFORMATION:

; APPLICANT: Farmacek, Michael S.

; APPLICANT: Solway, Julian

; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL

; TITLE OF INVENTION: EXPRESSION

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Arnold, White & Durkee

; STREET: P.O. Box 4433

; CITY: Houston

; STATE: Texas

; COUNTRY: USA

; ZIP: 77210

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/726,807B
FILING DATE: 07-OCT-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,868
FILING DATE: 05-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARSB:510
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 3..8
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "W = A or T"
US-08-726-807B-47

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWW 6
DB 2 CWW 4

RESULT 112
US-08-726-807B-47/c
Sequence 47, Application US/08726807B
Patent No. 6090618
GENERAL INFORMATION:
APPLICANT: Parmacek, Michael S.
APPLICANT: Solway, Julian
TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/726,807B
FILING DATE: 07-OCT-1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/004,868
FILING DATE: 05-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARSB:510
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: modified_base
LOCATION: 3..8
OTHER INFORMATION: /mod_base= OTHER
OTHER INFORMATION: /note= "W = A or T"
US-08-726-807B-47

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7
DB 4 WWG 2

RESULT 113
US-08-485-863A-23
Sequence 23, Application US/08485863A
Patent No. 6093548
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,863A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
DESCRIPTION: Initiator consensus sequence
US-08-485-863A-23

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
DB 1 YYY 3

RESULT 114
US-08-485-863A-23/c
; Sequence 23, Application US/08485863A
; Patent No. 6093548
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,863A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3G
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-435-2034
; TELEFAX: 415-435-0727
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
US-08-485-863A-23

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 10 RRR 8

RESULT 115
US-09-258-367-47
; Sequence 47, Application US/09258367
; Patent No. 6114311
; GENERAL INFORMATION:
; APPLICANT: PARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:310
; CURRENT APPLICATION NUMBER: US/09/258,367
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 08/726,807
; EARLIER FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47

; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-258-367-47

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWG 6
Db 2 CWG 4

RESULT 116
US-09-258-367-47/c
; Sequence 47, Application US/09258367
; Patent No. 6114311
; GENERAL INFORMATION:
; APPLICANT: PARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:310
; CURRENT APPLICATION NUMBER: US/09/258,367
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 08/726,807
; EARLIER FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-258-367-47

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7
Db 4 WWG 2

RESULT 117
US-08-972-927-11
; Sequence 11, Application US/08972927
; Patent No. 6166290
; GENERAL INFORMATION:
; APPLICANT: Rea, Philip A
; APPLICANT: Lu, Yu-Ping
; APPLICANT: Li, Ze-Sheng
; TITLE OF INVENTION: GLUTATHIONE-S-CONJUGATE TRANSPORT IN
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: One Commerce Square, 2005 Market Street, 22nd
; STREET: Floor

```

; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: US
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,927
; FILING DATE: 18-NOV-1997
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,040
; FILING DATE: 18-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/061,328
; FILING DATE: 08-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Doyle Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-12U2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; MOLECULE TYPE: DNA (genomic)
; US-08-972-927-11
;
; QUERY MATCH 30.0%; Score 3; DB 3; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 5 WWG 7
; DB 7 WWG 9
;
; RESULT 118
; US-08-972-927-11/c
; Sequence 11, Application US/08972927
; Patent No. 6166290
; GENERAL INFORMATION:
; APPLICANT: Rea, Philip A
; APPLICANT: Lu, Yu-Ping
; APPLICANT: Li, Ze-Sheng
; TITLE OF INVENTION: GLUTATHIONE-S-CONJUGATE TRANSPORT IN
; TITLE OF INVENTION: PLANTS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
; STREET: One Commerce Square, 2005 Market Street, 22nd
; STREET: Floor
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: US
; ZIP: 19103-7086
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/972,927
; FILING DATE: 18-NOV-1997
; CLASSIFICATION: 800

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/031,040
; FILING DATE: 18-NOV-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/061,328
; FILING DATE: 08-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Doyle Leary Ph.D., Kathryn
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: 9596-12U2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-965-1284
; TELEFAX: 215-567-2991
; MOLECULE TYPE: DNA (genomic)
; US-08-972-927-11
;
; QUERY MATCH 30.0%; Score 3; DB 3; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 CW 6
; DB 9 CW 7
;
; RESULT 119
; US-08-646-301A-11
; Sequence 11, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.
; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
; TITLE OF INVENTION: Antigen for Expression Targeting
; FILE REFERENCE: PB1508USM
; CURRENT APPLICATION NUMBER: US/08/646,301A
; CURRENT FILING DATE: 1996-05-16
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: consensus
; OTHER INFORMATION: sequence B12 from DNA Sequence 1:3-11 (1990).
; Patent No. 6194211
; US-08-646-301A-11
;
; QUERY MATCH 30.0%; Score 3; DB 3; Length 10;
; Best Local Similarity 100.0%; Pred. No. 0;
; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY 4 CW 6
; DB 2 CW 4
;
; RESULT 120
; US-08-646-301A-11/c
; Sequence 11, Application US/08646301A
; Patent No. 6194211
; GENERAL INFORMATION:
; APPLICANT: Richards, Cynthia Ann
; APPLICANT: Huber, Brian E.

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; TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic

; Patent No. 6194211

; TITLE OF INVENTION: Antigen for Expression Targeting

; FILE REFERENCE: PB1508USW

; CURRENT APPLICATION NUMBER: US/08/646,301A

; CURRENT FILING DATE: 1996-05-16

; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 10

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: consensus

; OTHER INFORMATION: sequence B12 from DNA Sequence 1:3-11 (1990).

; Patent No. 6194211

; US-08-646-301A-11

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 6

Db 9 CW 7

RESULT 121

US-08-485-049D-23

; Sequence 23, Application US/08485049D

; Patent No. 6204370

; GENERAL INFORMATION:

; APPLICANT: Zavada, Jan

; APPLICANT: Pastorekova, Silvia

; APPLICANT: Pastorek, Jaromir

; TITLE OF INVENTION: MN Gene and Protein

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leona L. Lauder

; STREET: 369 Pine Street

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/485,049D

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/260,190

; FILING DATE: 15-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863

; REFERENCE/DOCKET NUMBER: D-0021.3E

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-981-2034

; TELEFAX: 415-981-0332

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; DESCRIPTION: Initiator consensus sequence

US-08-485-049D-23

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 10

Db 1 YY 3

RESULT 122

US-08-485-049D-23/c

; Sequence 23, Application US/08485049D

; Patent No. 6204370

; GENERAL INFORMATION:

; APPLICANT: Zavada, Jan

; APPLICANT: Pastorekova, Silvia

; APPLICANT: Pastorek, Jaromir

; TITLE OF INVENTION: MN Gene and Protein

; NUMBER OF SEQUENCES: 86

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Leona L. Lauder

; STREET: 369 Pine Street

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94104

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/485,049D

; FILING DATE: 07-JUN-1995

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/260,190

; FILING DATE: 15-JUN-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Lauder, Leona L.

; REGISTRATION NUMBER: 30,863

; REFERENCE/DOCKET NUMBER: D-0021.3E

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-981-2034

; TELEFAX: 415-981-0332

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; DESCRIPTION: Initiator consensus sequence

US-08-485-049D-23

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3

Db 10 RRR 8

RESULT 123

US-09-134-246-1

; Sequence 1, Application US/09134246B

; Patent No. 6207377

; GENERAL INFORMATION:

; APPLICANT: Wayne, Jay

; APPLICANT: Xu, Shuang-yong

; TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle

; TITLE OF INVENTION: Vectors And Identification of Two Thermus Plasmid

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; TITLE OF INVENTION: Replication Origins
; FILE REFERENCE: Thermus Shuttle Vector
; CURRENT APPLICATION NUMBER: US/09/134,246B
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 30
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Thermus sp.
US-09-134-246-1

Query Match      30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RRC 4
Db      1 RRC 3

RESULT 124
US-09-134-246-1/c
; Sequence 1, Application US/09134246B
; Patent No. 6207377
; GENERAL INFORMATION:
; APPLICANT: Wayne, Jay
; TITLE OF INVENTION: Method For Construction Of Thermus-E. coli Shuttle
; TITLE OF INVENTION: Vectors And Identification Of Two Thermus Plasmid
; FILE REFERENCE: Replication Origins
; CURRENT APPLICATION NUMBER: US/09/134,246B
; CURRENT FILING DATE: 1998-08-14
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Thermus sp.
US-09-134-246-1

Query Match      30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
Db      10 RRR 8

RESULT 125
US-09-546-550-47
; Sequence 47, Application US/09546550
; Patent No. 6284743
; GENERAL INFORMATION:
; APPLICANT: PARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:310
; CURRENT APPLICATION NUMBER: US/09/546,550
; CURRENT FILING DATE: 2000-04-10
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; OTHER INFORMATION:

QY      1 RRR 3
Db      10 RRR 8

RESULT 126
US-09-546-550-47/c
; Sequence 47, Application US/09546550
; Patent No. 6284743
; GENERAL INFORMATION:
; APPLICANT: PARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:310
; CURRENT APPLICATION NUMBER: US/09/546,550
; CURRENT FILING DATE: 2000-04-10
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; OTHER INFORMATION:

QY      5 WWC 7
Db      4 WWC 2

RESULT 127
US-09-431-414-47
; Sequence 47, Application US/09431414
; Patent No. 6291211
; GENERAL INFORMATION:
; APPLICANT: PARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:335
; CURRENT APPLICATION NUMBER: US/09/431,414
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: 08/726,807
; PRIOR FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; OTHER INFORMATION:

QY      5 WWC 7
Db      4 WWC 2
```

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; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-546-550-47

Query Match      30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWW 6
Db      2 CWW 4

RESULT 126
US-09-546-550-47/c
; Sequence 47, Application US/09546550
; Patent No. 6284743
; GENERAL INFORMATION:
; APPLICANT: PARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:310
; CURRENT APPLICATION NUMBER: US/09/546,550
; CURRENT FILING DATE: 2000-04-10
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; OTHER INFORMATION:
; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-546-550-47

Query Match      30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WWC 7
Db      4 WWC 2

RESULT 127
US-09-431-414-47
; Sequence 47, Application US/09431414
; Patent No. 6291211
; GENERAL INFORMATION:
; APPLICANT: PARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:335
; CURRENT APPLICATION NUMBER: US/09/431,414
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: 08/726,807
; PRIOR FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; OTHER INFORMATION:
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; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-431-414-47

Query Match      30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CWG 6
      |||
Db      2 CWG 4

RESULT 128
US-09-431-414-47/c
; Sequence 47, Application US/09431414
; Patent No. 6291211
; GENERAL INFORMATION:
; APPLICANT: PHARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARCD:335
; CURRENT APPLICATION NUMBER: US/09/431,414
; CURRENT FILING DATE: 1999-11-01
; EARLIER APPLICATION NUMBER: 08/726,807
; EARLIER FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-431-414-47

Query Match      30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 WNG 7
      |||
Db      4 WNG 2

RESULT 129
US-09-178-115-23
; Sequence 23, Application US/09178115
; Patent No. 6297041
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5A
; CURRENT APPLICATION NUMBER: US/09/178,115
; CURRENT FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 09/177,776
; EARLIER FILING DATE: 1998-10-23
; EARLIER APPLICATION NUMBER: 08/787,739
; EARLIER FILING DATE: 1997-01-24
; EARLIER APPLICATION NUMBER: 08/485,049
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/486,756
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/477,504
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
; EARLIER APPLICATION NUMBER: 08/481,658
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,862
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/485,863
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/487,077
; EARLIER FILING DATE: 1995-06-07
; EARLIER APPLICATION NUMBER: 08/260,190
; EARLIER FILING DATE: 1994-06-15
; EARLIER APPLICATION NUMBER: 08/177,093
; EARLIER FILING DATE: 1993-12-30
; EARLIER APPLICATION NUMBER: 07/964,589
; EARLIER FILING DATE: 1992-10-21
; EARLIER APPLICATION NUMBER: PV-709-92
; EARLIER FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.0
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; OTHER INFORMATION: W = A or T
US-09-225-670-47

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWG 6
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Db 2 CWG 4

RESULT 134

US-09-225-670-47/c
; Sequence 47, Application US/09225670
; Patent No. 6297221
; GENERAL INFORMATION:
; APPLICANT: PHARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARSB:526
; CURRENT APPLICATION NUMBER: US/09/225,670
; CURRENT FILING DATE: 1999-01-05
; EARLIER FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-225-670-47

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7
|||
Db 4 WWG 2

RESULT 135

US-09-431-349C-47
; Sequence 47, Application US/09431349C
; Patent No. 6331527
; GENERAL INFORMATION:
; APPLICANT: PHARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARSB:526
; CURRENT APPLICATION NUMBER: US/09/431,349C
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/225,670
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: 08/726,807
; PRIOR FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Primer

; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-431-349C-47

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWG 6
|||
Db 2 CWG 4

RESULT 136

US-09-431-349C-47/c
; Sequence 47, Application US/09431349C
; Patent No. 6331527
; GENERAL INFORMATION:
; APPLICANT: PHARMACEK, MICHAEL S.
; APPLICANT: SOLWAY, JULIAN
; TITLE OF INVENTION: PROMOTER FOR SMOOTH MUSCLE CELL EXPRESSION
; FILE REFERENCE: ARSB:526
; CURRENT APPLICATION NUMBER: US/09/431,349C
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: 09/225,670
; PRIOR FILING DATE: 1999-01-05
; PRIOR APPLICATION NUMBER: 08/726,807
; PRIOR FILING DATE: 1996-10-07
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 47
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: modified_base
; LOCATION: (3)..(8)
; OTHER INFORMATION: W = A or T
US-09-431-349C-47

Query Match 30.0%; Score 3; DB 3; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7
|||
Db 4 WWG 2

RESULT 137

US-09-122-171D-3
; Sequence 3, Application US/09122171D
; Patent No. 6423693
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: Draghia-Akli, Ruxandra
; APPLICANT: Li, Xuyang
; APPLICANT: Eastman, Eric
; TITLE OF INVENTION: GHRH Expression System and Methods of Use
; FILE REFERENCE: 236/006 GeneMedicine
; CURRENT APPLICATION NUMBER: US/09/122,171D
; CURRENT FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 60/062,608
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: 60/053,609
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10

; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: The inner core of the serum response element
; NAME/KEY: misc.feature
; LOCATION: (3)..(8)
; OTHER INFORMATION: The letter "w" stands for a or t
US-09-122-171D-3

Query Match 30.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
|||
Db 2 CWW 4

RESULT 138
US-09-122-171D-3/c
; Sequence 3, Application US/09122171D
; Patent No. 6423693
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: Draghita-Akli, Ruxandra
; APPLICANT: Li, Xuyang
; APPLICANT: Eastman, Eric
; TITLE OF INVENTION: GHRH Expression System and Methods of Use
; FILE REFERENCE: 236/006 GeneMedicine
; CURRENT APPLICATION NUMBER: US/09/122,171D
; CURRENT FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 60/062,608
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: 60/053,609
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: The inner core of the serum response element
; NAME/KEY: misc.feature
; LOCATION: (3)..(8)
; OTHER INFORMATION: The letter "w" stands for a or t
US-09-122-171D-3

Query Match 30.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
|||
Db 9 CWW 7

RESULT 139
US-09-772-719B-23
; Sequence 23, Application US/09772719B
; Patent No. 6770438
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; Pastorekova, Silvia
; Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 465 California Street, Suite 450
; CITY: San Francisco
; STATE: California
; COUNTRY: USA

; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719B
; FILING DATE: 30-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3A-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-772-719B-23

Query Match 30.0%; Score 3; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 1 YYY 3

RESULT 140
US-09-772-719B-23/c
; Sequence 23, Application US/09772719B
; Patent No. 6770438
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; Pastorekova, Silvia
; Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 465 California Street, Suite 450
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719B
; FILING DATE: 30-Jan-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3A-2

TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-981-2034

; TELEFAX: 415-981-0332

; INFORMATION FOR SEQ ID NO: 23:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 10 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; DESCRIPTION: Initiator consensus sequence

; SEQUENCE DESCRIPTION: SEQ ID NO: 23:

US-09-772-719B-23

Query Match 30.0%; Score 3; DB 4; Length 10;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3

Db 10 RRR 8

RESULT 141

5164316-1

; Patent No. 5164316

; APPLICANT: MCPHERSON, JOAN C.; KAY, ROBERT

; TITLE OF INVENTION: DNA CONSTRUCT FOR ENHANCING THE

; EFFICIENCY OF TRANSCRIPTION

; NUMBER OF SEQUENCES: 1

; CURRENT APPLICATION DATA:

; FILING DATE: 17-AUG-1989

; PRIOR APPLICATION NUMBER: 147,887

; FILING DATE: 25-JAN-1988

; APPLICATION NUMBER: 2,780

; FILING DATE: 13-JAN-1987

; SEQ ID NO: 1:

; LENGTH: 10

5164316-1

Query Match 30.0%; Score 3; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WWG 7

Db 8 WWG 10

RESULT 142

5164316-1/c

; Patent No. 5164316

; APPLICANT: MCPHERSON, JOAN C.; KAY, ROBERT

; TITLE OF INVENTION: DNA CONSTRUCT FOR ENHANCING THE

; EFFICIENCY OF TRANSCRIPTION

; NUMBER OF SEQUENCES: 1

; CURRENT APPLICATION DATA:

; FILING DATE: 17-AUG-1989

; PRIOR APPLICATION NUMBER: 147,887

; FILING DATE: 25-JAN-1988

; APPLICATION NUMBER: 2,780

; FILING DATE: 13-JAN-1987

; SEQ ID NO: 1:

; LENGTH: 10

5164316-1

Query Match 30.0%; Score 3; DB 6; Length 10;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWG 6

Db 10 CWG 8

RESULT 143

US-08-643-886-13

; Sequence 13, Application US/08643886

; Patent No. 5695977

; GENERAL INFORMATION:

; APPLICANT: JURKA, Jerzy W.

; TITLE OF INVENTION: Site Directed Recombination

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: US

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/643,886

; FILING DATE:

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Rowland, Bertram I

; REGISTRATION NUMBER: 20015

; REFERENCE/DOCKET NUMBER: A-63252/BIR

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-781-1989

; TELEFAX: 415-398-3249

; INFORMATION FOR SEQ ID NO: 13:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: other nucleic acid

; DESCRIPTION: /desc = "sequence"

US-08-643-886-13

Query Match 30.0%; Score 3; DB 1; Length 11;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3

Db 8 RRR 10

RESULT 144

US-08-643-886-13/c

; Sequence 13, Application US/08643886

; Patent No. 5695977

; GENERAL INFORMATION:

; APPLICANT: JURKA, Jerzy W.

; TITLE OF INVENTION: Site Directed Recombination

; NUMBER OF SEQUENCES: 22

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert

; STREET: Four Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: US

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,886
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-63252/BIR
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "sequence"
US-08-643-886-13

Query Match 30.0%; Score 3; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
|||
Db 10 YYY 8

RESULT 145
US-08-643-886-2
Sequence 2, Application US/08643886
Patent No. 5695977
GENERAL INFORMATION:
APPLICANT: JURKA, Jerzy W.
TITLE OF INVENTION: Site Directed Recombination
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,886
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-63252/BIR
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "sequence"
US-08-643-886-2

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
|||
Db 9 YYY 11

RESULT 146
US-08-643-886-2/c
Sequence 2, Application US/08643886
Patent No. 5695977
GENERAL INFORMATION:
APPLICANT: JURKA, Jerzy W.
TITLE OF INVENTION: Site Directed Recombination
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: US
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,886
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertram I
REGISTRATION NUMBER: 20015
REFERENCE/DOCKET NUMBER: A-63252/BIR
TELEPHONE: 415-781-1989
TELEFAX: 415-398-3249
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "sequence"
US-08-643-886-2

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
|||
Db 11 RRR 9

RESULT 147
US-08-643-886-14
Sequence 14, Application US/08643886
Patent No. 5695977
GENERAL INFORMATION:
APPLICANT: JURKA, Jerzy W.
TITLE OF INVENTION: Site Directed Recombination
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA


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; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
US-08-643-886-14

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 9 RRR 11

RESULT 148
US-08-643-886-14/c
; Sequence 14, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/08/643,886
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
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; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
US-08-643-886-14

Query Match 30.0%; Score 3; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 11 YYY 9

RESULT 149
US-08-235-503B-33
; Sequence 33, Application US/08235503B
; Patent No. 5563036
; GENERAL INFORMATION:
; APPLICANT: Peterson, Michael G
; APPLICANT: Baichwal, Vijay R
; APPLICANT: Strulovici, Berta
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 29-APR-1994
; APPLICATION NUMBER: US/08/235,503B
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59332/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-235-503B-33

Query Match 30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 11 YYY 13

RESULT 150
US-08-235-503B-33/c
; Sequence 33, Application US/08235503B
; Patent No. 5563036
; GENERAL INFORMATION:
; APPLICANT: Peterson, Michael G
; APPLICANT: Baichwal, Vijay R
```

```

; APPLICANT: Strulovici, Berta
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA ASSAY
; NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 29-APR-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: A-59332/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-235-503B-33

```

```

Query Match          30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 RRR 3
DB      13 RRR 11

```

```

RESULT 151
US-08-643-886-3
; Sequence 3, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR

```

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
; US-08-643-886-3

```

```

Query Match          30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      8 YYY 10
DB      10 YYY 12

```

```

RESULT 152
US-08-643-886-3/c
; Sequence 3, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
; US-08-643-886-3

```

```

Query Match          30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 RRR 3
DB      12 RRR 10

```

RESULT 153

US-08-643-886-15
; Sequence 15, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
US-08-643-886-15
Query Match 30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRR 3
Db 10 RRR 12
RESULT 154
US-08-643-886-15/c
; Sequence 15, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
US-08-643-886-15
Query Match 30.0%; Score 3; DB 1; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 YYY 10
Db 12 YYY 10
RESULT 155
PCT-US95-05265-33
; Sequence 33, Application PC/TUS9505265
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05265
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,503
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
PCT-US95-05265-33
Query Match 30.0%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YY 10
Db 11 YY 13

RESULT 156
PCT-US95-05265-33/c
; Sequence 33, Application PC/TUS9505265
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: TRANSCRIPTION FACTOR-DNA BINDING ASSAY
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05265
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/235,503
; FILING DATE: 29-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: PP-59232-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; PCT-US95-05265-33

Query Match 30.0%; Score 3; DB 5; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 13 RRR 11

RESULT 157
US-07-882-838E-32
; Sequence 32, Application US/07882838E
; Patent No. 5616461
; GENERAL INFORMATION:
; APPLICANT: Priscilla A. Schaffer
; APPLICANT: Christine E. Dabrowski Amaral
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; STREET: One Liberty Place
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.

; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,838E
; FILING DATE: May 14, 1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathryn Leary
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: DFCI-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100
; TELEFAX: (215) 568-3439
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-882-838E-32

Query Match 30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
Db 8 RRC 10

RESULT 158
US-07-882-838E-32/c
; Sequence 32, Application US/07882838E
; Patent No. 5616461
; GENERAL INFORMATION:
; APPLICANT: Priscilla A. Schaffer
; APPLICANT: Christine E. Dabrowski Amaral
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR
; TREATMENT OF VIRUS INFECTIONS
; NUMBER OF SEQUENCES: 49
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn
; STREET: One Liberty Place
; CITY: Philadelphia
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 50Z or 55SX
; OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/882,838E
; FILING DATE: May 14, 1992
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Kathryn Leary
; REGISTRATION NUMBER: 36,317
; REFERENCE/DOCKET NUMBER: DFCI-0001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 568-3100

```
;
; TELEFAX: (215) 568-3439
; TELEX:
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-07-882-838E-32

Query Match 30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GY 9
   |||
Db 10 GY 8

RESULT 159
US-08-643-886-4
; Sequence 4, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
; US-08-643-886-4

Query Match 30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
   |||
Db 13 RRR 11

RESULT 161
US-08-643-886-16
; Sequence 16, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
; US-08-643-886-4

Query Match 30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
   |||
Db 11 YYY 13

RESULT 160
US-08-643-886-4/c
; Sequence 4, Application US/08643886
; Patent No. 5695977
```

/ REFERENCE/DOCKET NUMBER: A-63252/BIR
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-781-1989
/ TELEFAX: 415-398-3249
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "sequence"
US-08-643-886-16

Query Match 30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 11 RRR 13

RESULT 162
US-08-643-886-16/c
/ Sequence 16, Application US/08643886
/ Patent No. 5695977
/ GENERAL INFORMATION:
/ APPLICANT: JURKA, Jerzy W.
/ TITLE OF INVENTION: Site Directed Recombination
/ NUMBER OF SEQUENCES: 22
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Flehr, Hohnbach, Test, Albritton & Herbert
/ STREET: Four Embarcadero Center, Suite 3400
/ CITY: San Francisco
/ STATE: CA
/ COUNTRY: US
/ ZIP: 94111
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/643,886
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Rowland, Bertram I
/ REGISTRATION NUMBER: 20015
/ REFERENCE/DOCKET NUMBER: A-63252/BIR
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-781-1989
/ TELEFAX: 415-398-3249
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "sequence"
US-08-643-886-16

Query Match 30.0%; Score 3; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 13 YYY 11

RESULT 163
US-08-646-789A-38
/ Sequence 38, Application US/08646789A
/ Patent No. 6022863
/ GENERAL INFORMATION:
/ APPLICANT: Peyman, John A.
/ TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
/ NUMBER OF SEQUENCES: 101
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: PENNIE & EDMONDS
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/646,789A
/ FILING DATE: May 21, 1996
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Misrock, S. Leslie
/ REGISTRATION NUMBER: 18,872
/ REFERENCE/DOCKET NUMBER: 6523-006
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-9741/8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 38:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA
US-08-646-789A-38

Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 11 YYY 13

RESULT 164
US-08-646-789A-38/c
/ Sequence 38, Application US/08646789A
/ Patent No. 6022863
/ GENERAL INFORMATION:
/ APPLICANT: Peyman, John A.
/ TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
/ NUMBER OF SEQUENCES: 101
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: PENNIE & EDMONDS
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: U.S.A.
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/646,789A
/ FILING DATE: May 21, 1996

CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 38:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-646-789A-38

Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3

DB 14 RRR 12

RESULT 165
US-08-646-789A-39
Sequence 39, Application US/08646789A
Patent No. 6022863
GENERAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: May 21, 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-646-789A-39

Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3

DB 1 RRR 3
RESULT 166
US-08-646-789A-39/c
Sequence 39, Application US/08646789A
Patent No. 6022863
GENERAL INFORMATION:
APPLICANT: Peyman, John A.
TITLE OF INVENTION: REGULATION OF GENE EXPRESSION
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,789A
FILING DATE: May 21, 1996
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6523-006
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-646-789A-39

Query Match 30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10

DB 4 YYY 2

RESULT 167
US-08-646-301A-8
Sequence 8, Application US/08646301A
Patent No. 6194211
GENERAL INFORMATION:
APPLICANT: Richards, Cynthia Ann
APPLICANT: Huber, Brian E.
TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
Antigen for Expression Targeting
Patent No. 6194211
TITLE OF INVENTION: Antigen for Expression Targeting
FILE REFERENCE: P61508USW
CURRENT APPLICATION NUMBER: US/08/646,301A
CURRENT FILING DATE: 1996-05-16
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 8
LENGTH: 14
TYPE: DNA
ORGANISM: Artificial Sequence

```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: consensus
/ OTHER INFORMATION: sequence A4alt from DNA Sequence 1:3-11 (1990).
/ Patent No. 6194211
US-08-646-301A-8

Query Match          30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
   |||
Db 1 RRR 3

RESULT 168
US-08-646-301A-8/c
/ Sequence 8, Application US/08646301A
/ Patent No. 6194211
/ GENERAL INFORMATION:
/ APPLICANT: Richards, Cynthia Ann
/ APPLICANT: Huber, Brian E.
/ TITLE OF INVENTION: Transcriptional Regulatory Sequence of Carcinoembryonic
/ Patent No. 6194211
/ TITLE OF INVENTION: Antigen for Expression Targeting
/ FILE REFERENCE: PB1508USW
/ CURRENT APPLICATION NUMBER: US/08/646,301A
/ CURRENT FILING DATE: 1996-05-16
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 14
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: consensus
/ OTHER INFORMATION: sequence A4alt from DNA Sequence 1:3-11 (1990).
/ Patent No. 6194211
US-08-646-301A-8

Query Match          30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
   |||
Db 3 YYY 1

RESULT 169
US-09-305-639-7
/ Sequence 7, Application US/09305639
/ Patent No. 6200778
/ GENERAL INFORMATION:
/ APPLICANT: Treco, Douglas A.
/ APPLICANT: Heartlein, Michael W.
/ APPLICANT: Seiden, Richard F.
/ TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
/ FILE REFERENCE: 07236/016001
/ CURRENT APPLICATION NUMBER: US/09/305,639
/ CURRENT FILING DATE: 1999-05-05
/ EARLIER APPLICATION NUMBER: 60/084,663
/ EARLIER FILING DATE: 1998-05-07
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 7
/ LENGTH: 14
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(14)
/ OTHER INFORMATION: n = A,T,C or G
US-09-305-639-7

Query Match          30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
   |||
Db 1 YYY 3

RESULT 170
US-09-305-639-7/c
/ Sequence 7, Application US/09305639
/ Patent No. 6200778
/ GENERAL INFORMATION:
/ APPLICANT: Treco, Douglas A.
/ APPLICANT: Heartlein, Michael W.
/ APPLICANT: Seiden, Richard F.
/ TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
/ FILE REFERENCE: 07236/016001
/ CURRENT APPLICATION NUMBER: US/09/305,639
/ CURRENT FILING DATE: 1999-05-05
/ EARLIER APPLICATION NUMBER: 60/084,663
/ EARLIER FILING DATE: 1998-05-07
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 7
/ LENGTH: 14
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(14)
/ OTHER INFORMATION: n = A,T,C or G
US-09-305-639-7

Query Match          30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
   |||
Db 10 RRR 8

RESULT 171
US-09-305-384-8
/ Sequence 8, Application US/09305384
/ Patent No. 6242218
/ GENERAL INFORMATION:
/ APPLICANT: Treco, Douglas A.
/ APPLICANT: Heartlein, Michael W.
/ APPLICANT: Seiden, Richard F.
/ TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
/ FILE REFERENCE: 07236/017001
/ CURRENT APPLICATION NUMBER: US/09/305,384
/ CURRENT FILING DATE: 1999-05-05
/ EARLIER APPLICATION NUMBER: US 60/084,649
/ EARLIER FILING DATE: 1998-05-07
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 8
/ LENGTH: 14
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)...(14)
/ OTHER INFORMATION: n = A,T,C or G
US-09-305-384-8

Query Match          30.0%; Score 3; DB 3; Length 14;
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
      |||
Db      1 YYY 3

RESULT 172
US-09-305-384-8/c
; Sequence 8, Application US/09305384
; Patent No. 6242218
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 072367017001
; CURRENT APPLICATION NUMBER: US/09/305,384
; CURRENT FILING DATE: 1999-05-05
; EARLIER APPLICATION NUMBER: US 60/084,649
; EARLIER FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(14)
; OTHER INFORMATION: n = A,T,C or G
US-09-305-384-8

Query Match      30.0%; Score 3; DB 3; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
      |||
Db      10 RRR 8

RESULT 173
US-09-318-138-22
; Sequence 22, Application US/09318138
; Patent No. 6531123
; GENERAL INFORMATION:
; APPLICANT: CHANG, Lung-Ji
; TITLE OF INVENTION: LENTIVIRAL VECTORS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/318,138
; FILING DATE: 25-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/086,635
; FILING DATE: 26-MAY-1998
; APPLICATION NUMBER: US 08/935,312
; FILING DATE: 22-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: CHANG=109A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-318-138-22

Query Match      30.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
      |||
Db      1 YYY 3

US-09-318-138-22
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: CHANG=109A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-318-138-22

Query Match      30.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
      |||
Db      1 YYY 3

RESULT 174
US-09-318-138-22/c
; Sequence 22, Application US/09318138
; Patent No. 6531123
; GENERAL INFORMATION:
; APPLICANT: CHANG, Lung-Ji
; TITLE OF INVENTION: LENTIVIRAL VECTORS
; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/318,138
; FILING DATE: 25-May-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/086,635
; FILING DATE: 26-MAY-1998
; APPLICATION NUMBER: US 08/935,312
; FILING DATE: 22-SEP-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: CHANG=109A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-318-138-22

Query Match      30.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
|||
Db 10 RRR 8

RESULT 175

US-09-525-160B-10
; Sequence 10, Application US/09525160B
; Patent No. 6569681
; GENERAL INFORMATION:
; APPLICANT: Ivanov, Evguenii
; TITLE OF INVENTION: METHODS OF IMPROVING HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 10278/016001
; CURRENT APPLICATION NUMBER: US/09/525,160B
; CURRENT FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n = a, g, c or t
US-09-525-160B-10

Query Match 30.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
|||
Db 1 YYY 3

RESULT 176

US-09-525-160B-10/c
; Sequence 10, Application US/09525160B
; Patent No. 6569681
; GENERAL INFORMATION:
; APPLICANT: Ivanov, Evguenii
; TITLE OF INVENTION: METHODS OF IMPROVING HOMOLOGOUS RECOMBINATION
; FILE REFERENCE: 10278/016001
; CURRENT APPLICATION NUMBER: US/09/525,160B
; CURRENT FILING DATE: 2000-03-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetically generated oligonucleotide
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n = a, g, c or t
US-09-525-160B-10

Query Match 30.0%; Score 3; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
|||
Db 10 RRR 8

RESULT 177

PCT-US94-06456-4
; Sequence 4, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine
PCT-US94-06456-4

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
|||
Db 12 RRR 14

RESULT 178

PCT-US94-06456-4/c
; Sequence 4, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
PCT-US94-06456-4

```
;
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine
;
PCT-US94-06456-4

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 10
Db 14 YY 12

RESULT 179
PCT-US94-06456-33
; Sequence 33, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine.
;
PCT-US94-06456-33

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 10
Db 14 YY 12

RESULT 179
PCT-US94-06456-33
; Sequence 33, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine.
;
PCT-US94-06456-33

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 10
Db 14 YY 12
```

```
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine.
;
PCT-US94-06456-33

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 12 RRR 14

RESULT 180
PCT-US94-06456-33/c
; Sequence 33, Application PC/TUS9406456
; GENERAL INFORMATION:
; APPLICANT: Beutel, Bruce A.
; APPLICANT: Coppola, George R.
; APPLICANT: Sherman, Michael I.
; TITLE OF INVENTION: Oligonucleotides Which Inhibit HIV Protease Function
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carelia, Byrne, Bain, Gilfillan, Cecchi, Stewart & Olstein
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC - DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/06456
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/073,873
; FILING DATE: 09-JUN-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliott M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 23550-89
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 33:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: oligonucleotide
; FEATURE:
; OTHER INFORMATION: R is a modified or unmodified purine.
;
PCT-US94-06456-33

Query Match 30.0%; Score 3; DB 5; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 10
Db 14 YY 12
```

RESULT 181
US-08-643-886-5
; Sequence 5, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/643,886
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
US-08-643-886-5

Query Match 30.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 12 YYY 14

RESULT 182
US-08-643-886-5/c
; Sequence 5, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886

; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
US-08-643-886-5
Query Match 30.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 14 RRR 12

RESULT 183
US-08-643-886-17
; Sequence 17, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: US/08/643,886
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
US-08-643-886-17

Query Match 30.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 12 RRR 14

RESULT 184

US-08-643-886-17/c
; Sequence 17, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"

Query Match 30.0%; Score 3; DB 1; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 14 YYY 12

RESULT 185

US-08-737-371A-8
; Sequence 8, Application US/08737371A
; Patent No. 5959094
; GENERAL INFORMATION:
; APPLICANT: David WALLACH
; APPLICANT: Peter KUHNERT
; APPLICANT: Gotz EHRHARDT
; APPLICANT: Oliver KEMPER
; TITLE OF INVENTION: p75 TNF RECEPTOR PROMOTERS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,371A
; FILING DATE: 08-NOVEMBER-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05853
; FILING DATE: 11-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109,633
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: WALLACH=14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

US-08-737-371A-8
Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 1 YYY 3

RESULT 186

US-08-737-371A-8/c
; Sequence 8, Application US/08737371A
; Patent No. 5959094
; GENERAL INFORMATION:
; APPLICANT: David WALLACH
; APPLICANT: Peter KUHNERT
; APPLICANT: Gotz EHRHARDT
; APPLICANT: Oliver KEMPER
; TITLE OF INVENTION: p75 TNF RECEPTOR PROMOTERS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/737,371A
; FILING DATE: 08-NOVEMBER-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/05853
; FILING DATE: 11-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 109,633
; FILING DATE: 11-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.

/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: WALLACH=14
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: cDNA
US-08-737-371A-8

Query Match 30.0%; Score 3; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 11 RRR 9

RESULT 187
US-08-256-004-4
; Sequence 4, Application US/08256004
; Patent No. 6001644
; GENERAL INFORMATION:
; APPLICANT: Robert J. Debs
; APPLICANT: Ning Zhu
; TITLE OF INVENTION: IN VIVO TRANSFECTION WITH A CFTR CODING
; TITLE OF INVENTION: SEQUENCE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94306-2155

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,004
; FILING DATE: August 22, 1994
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/11004
; FILING DATE: December 17, 1992
; APPLICATION NUMBER: 07/972,135
; FILING DATE: No. 6001644ember 5, 1992
; APPLICATION NUMBER: 07/927,200
; FILING DATE: August 6, 1992
; APPLICATION NUMBER: 07/894,498
; FILING DATE: June 4, 1992

ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCSF-008/0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5070
; TELEFAX: (415) 857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single

Query Match 30.0%; Score 3; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 11 RRR 9

/ TOPOLOGY: linear
US-08-256-004-4
Query Match 30.0%; Score 3; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 8 YYY 10
Db 1 YYY 3

RESULT 188
US-08-256-004-4/c
; Sequence 4, Application US/08256004
; Patent No. 6001644
; GENERAL INFORMATION:
; APPLICANT: Robert J. Debs
; APPLICANT: Ning Zhu
; TITLE OF INVENTION: IN VIVO TRANSFECTION WITH A CFTR CODING
; TITLE OF INVENTION: SEQUENCE
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooley Godward Castro Huddleson & Tatum
; STREET: 5 Palo Alto Square
; CITY: Palo Alto
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 94306-2155

COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/256,004
; FILING DATE: August 22, 1994
; CLASSIFICATION: 514

PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/11004
; FILING DATE: December 17, 1992
; APPLICATION NUMBER: 07/972,135
; FILING DATE: No. 6001644ember 5, 1992
; APPLICATION NUMBER: 07/927,200
; FILING DATE: August 6, 1992
; APPLICATION NUMBER: 07/894,498
; FILING DATE: June 4, 1992

ATTORNEY/AGENT INFORMATION:
; NAME: Neeley, Richard L.
; REGISTRATION NUMBER: 30,092
; REFERENCE/DOCKET NUMBER: UCSF-008/0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 843-5070
; TELEFAX: (415) 857-0663
; TELEX: 380816COOLEYPA
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear

US-08-256-004-4
Query Match 30.0%; Score 3; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 189
US-09-461-686-3
; Sequence 3, Application US/09461686
; Patent No. 6620795
; GENERAL INFORMATION:
; APPLICANT: Debs, Robert J.
;           Zhu, Ning
; TITLE OF INVENTION: A Mammalian Transformation Complex
;           Comprising a Lipid Carrier and DNA Encoding CPTP
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,686
; FILING DATE: 14-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/256,004
; FILING DATE: 22-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Mycroft, Frank J.
; REGISTRATION NUMBER: 46,946
; REFERENCE/DOCKET NUMBER: 023070-064710US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-461-686-3
Query Match 30.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 190
US-09-461-686-3/C
; Sequence 3, Application US/09461686
; Patent No. 6620795
; GENERAL INFORMATION:
; APPLICANT: Debs, Robert J.
;           Zhu, Ning
; TITLE OF INVENTION: A Mammalian Transformation Complex
;           Comprising a Lipid Carrier and DNA Encoding CPTP
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/461,686
FILING DATE: 14-Dec-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,004
FILING DATE: 22-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Mycroft, Frank J.
REGISTRATION NUMBER: 46,946
REFERENCE/DOCKET NUMBER: 023070-064710US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-461-686-3
Query Match 30.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 10 RRR 8

RESULT 191
US-09-586-216C-5
; Sequence 5, Application US/09586216C
; Patent No. 6696272
; GENERAL INFORMATION:
; APPLICANT: MAHURAN, Don J.
; APPLICANT: CLARKE, Joe T.R.
; APPLICANT: CALLAHAN, John W.
; TITLE OF INVENTION: PRODUCTS AND METHODS FOR GAUCHER DISEASE THERAPY
; FILE REFERENCE: 24,131 USA
; CURRENT APPLICATION NUMBER: US/09/586,216C
; CURRENT FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/137,598
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 2,272,055
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: Y=1-10; n=11
; OTHER INFORMATION: y=c or u; n=any nucleotide
US-09-586-216C-5
Query Match 30.0%; Score 3; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3
```

RESULT 192
 US-09-586-216C-5/c
 ; Sequence 5, Application US/09586216C
 ; Patent No. 6696272
 ; GENERAL INFORMATION:
 ; APPLICANT: MAHURAN, Don J.
 ; APPLICANT: CLARKE, Joe T.R.
 ; APPLICANT: CALLAHAN, John W.
 ; TITLE OF INVENTION: PRODUCTS AND METHODS FOR GAUCHER DISEASE THERAPY
 ; FILE REFERENCE: 24,131 USA
 ; CURRENT APPLICATION NUMBER: US/09/586,216C
 ; CURRENT FILING DATE: 2000-06-02
 ; PRIOR APPLICATION NUMBER: 60/137,598
 ; PRIOR FILING DATE: 1999-06-03
 ; PRIOR APPLICATION NUMBER: 2,272,055
 ; PRIOR FILING DATE: 1999-06-02
 ; NUMBER OF SEQ ID NOS: 19
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 15
 ; TYPE: RNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc_difference
 ; LOCATION: y=1-10; n=11
 ; OTHER INFORMATION: y=c or u; n=any nucleotide
 US-09-586-216C-5

Query Match 30.0%; Score 3; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
 Db 10 RRR 8

RESULT 193
 PCT-US95-05853-8
 ; Sequence 8, Application PC/TUS9505853
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: p75 TNF RECEPTOR PROMOTERS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/05853
 ; FILING DATE: 11-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: IL 109,633
 ; FILING DATE: 11-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: WALLACH=14 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 PCT-US95-05853-8
 Query Match 30.0%; Score 3; DB 5; Length 15;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
 Db 1 YYY 3

RESULT 194
 PCT-US95-05853-8/c
 ; Sequence 8, Application PC/TUS9505853
 ; GENERAL INFORMATION:
 ; APPLICANT:
 ; TITLE OF INVENTION: p75 TNF RECEPTOR PROMOTERS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BROWDY AND NEIMARK
 ; STREET: 419 Seventh Street, N.W., Suite 300
 ; CITY: Washington
 ; STATE: D.C.
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US95/05853
 ; FILING DATE: 11-MAY-1995
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: IL 109,633
 ; FILING DATE: 11-MAY-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROWDY, Roger L.
 ; REGISTRATION NUMBER: 25,618
 ; REFERENCE/DOCKET NUMBER: WALLACH=14 PCT
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 202-628-5197
 ; TELEFAX: 202-737-3528
 ; TELEX: 248633
 ; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
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Qy 1 RRR 3
 Db 11 RRR 9

RESULT 195
 US-08-486-421-32
 ; Sequence 32, Application US/08486421
 ; Patent No. 5672479
 ; GENERAL INFORMATION:

;; APPLICANT: Johnson, Edward M.
;; APPLICANT: Bergemann, Andrew D.
;; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
;; NUMBER OF SEQUENCES: 51
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/486,421
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/470,911
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 6923-053
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 32:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
US-08-486-421-32
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRR 3
Db 13 RRR 15
RESULT 196
US-08-486-421-32/c
; Sequence 32, Application US/08486421
; Patent No. 5672479
; GENERAL INFORMATION:
; APPLICANT: Johnson, Edward M.
; APPLICANT: Bergemann, Andrew D.
; TITLE OF INVENTION: CLONING AND EXPRESSION OF PUR PROTEIN
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,421
; FILING DATE: 07-JUN-1995

;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/470,911
;; FILING DATE: 06-JUN-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Coruzzi, Laura A.
;; REGISTRATION NUMBER: 30,742
;; REFERENCE/DOCKET NUMBER: 6923-053
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 32:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: unknown
;; MOLECULE TYPE: DNA (genomic)
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; Sequence 6, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 6:
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Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 YYY 15

RESULT 198

US-08-643-886-6/c
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; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
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; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
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US-08-643-886-6

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; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
US-08-643-886-18

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 13 RRR 15

RESULT 200

US-08-643-886-18/c
; Sequence 18, Application US/08643886
; Patent No. 5695977
; GENERAL INFORMATION:
; APPLICANT: JURKA, Jerzy W.
; TITLE OF INVENTION: Site Directed Recombination
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hobbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: US
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/643,886
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertram I
; REGISTRATION NUMBER: 20015
; REFERENCE/DOCKET NUMBER: A-63252/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-781-1989
; TELEFAX: 415-398-3249
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "sequence"
US-08-643-886-18

US-08-643-886-18

Query Match 30.0%; Score 3; DB 1; Length 16;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
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Db 15 YYY 13

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OM nucleic - nucleic search, using sw model

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Perfect score: 10
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Minimum DB seq length: 0
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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C 107	3	30.0	6	16	US-10-437-263-27	Sequence 27, Appl	C 180	3	30.0	16	9	US-09-836-866-7	Sequence 5, Appl
C 108	3	30.0	6	16	US-10-437-275-27	Sequence 27, Appl	C 181	3	30.0	17	9	US-09-892-867-5	Sequence 15, Appl
C 109	3	30.0	6	16	US-10-437-275-27	Sequence 27, Appl	C 182	3	30.0	17	9	US-09-892-867-5	Sequence 15, Appl
C 110	3	30.0	6	16	US-10-437-258-27	Sequence 27, Appl	C 183	3	30.0	17	9	US-09-973-451-15	Sequence 4, Appl
C 111	3	30.0	8	9	US-09-816-763-16	Sequence 16, Appl	C 184	3	30.0	17	9	US-09-973-451-15	Sequence 4, Appl
C 112	3	30.0	8	9	US-09-816-763-16	Sequence 16, Appl	C 185	3	30.0	17	10	US-09-836-705-4	Sequence 5, Appl
C 113	3	30.0	8	9	US-09-816-763-32	Sequence 32, Appl	C 186	3	30.0	17	10	US-09-836-705-4	Sequence 5, Appl
C 114	3	30.0	8	9	US-09-816-763-32	Sequence 32, Appl	C 187	3	30.0	17	10	US-09-903-770-5	Sequence 10, Appl
C 115	3	30.0	8	10	US-09-798-883B-56	Sequence 56, Appl	C 188	3	30.0	17	10	US-09-903-770-5	Sequence 10, Appl
C 116	3	30.0	8	10	US-09-798-883B-56	Sequence 56, Appl	C 189	3	30.0	17	11	US-09-876-813-10	Sequence 4, Appl
C 117	3	30.0	8	10	US-09-326-885-56	Sequence 56, Appl	C 190	3	30.0	17	11	US-09-876-813-10	Sequence 5, Appl
C 118	3	30.0	8	10	US-09-326-885-56	Sequence 56, Appl	C 191	3	30.0	17	11	US-10-043-142-1	Sequence 10, Appl
C 119	3	30.0	8	15	US-10-253-117-3	Sequence 3, Appl	C 192	3	30.0	17	13	US-10-043-142-1	Sequence 1, Appl
C 120	3	30.0	8	15	US-10-253-117-3	Sequence 3, Appl	C 193	3	30.0	17	13	US-10-139-583-10	Sequence 1, Appl
C 121	3	30.0	8	15	US-10-253-117-3	Sequence 3, Appl	C 194	3	30.0	17	13	US-10-139-583-10	Sequence 10, Appl
C 122	3	30.0	8	15	US-10-253-117-4	Sequence 4, Appl	C 195	3	30.0	17	13	US-10-338-237-16	Sequence 10, Appl
C 123	3	30.0	8	15	US-10-253-117-4	Sequence 4, Appl	C 196	3	30.0	17	15	US-10-338-237-16	Sequence 16, Appl
C 124	3	30.0	8	17	US-10-821-568-32	Sequence 32, Appl	C 197	3	30.0	17	15	US-10-302-554-29	Sequence 29, Appl
C 125	3	30.0	8	17	US-10-821-568-32	Sequence 32, Appl	C 198	3	30.0	17	15	US-10-302-554-29	Sequence 29, Appl
C 126	3	30.0	10	9	US-09-772-719-23	Sequence 23, Appl	C 199	3	30.0	17	15	US-10-404-300A-28	Sequence 28, Appl
C 127	3	30.0	10	9	US-09-772-719-23	Sequence 23, Appl	C 200	3	30.0	17	15	US-10-404-300A-28	Sequence 28, Appl
C 128	3	30.0	10	10	US-09-967-237-23	Sequence 23, Appl	C 201	3	30.0	17	17	US-10-727-516-5	Sequence 5, Appl
C 129	3	30.0	10	10	US-09-967-237-23	Sequence 23, Appl	C 202	3	30.0	17	17	US-10-727-516-5	Sequence 5, Appl
C 130	3	30.0	10	14	US-10-124-759-3	Sequence 3, Appl	C 203	3	30.0	17	18	US-10-877-623-10	Sequence 10, Appl
C 131	3	30.0	10	14	US-10-124-759-3	Sequence 3, Appl	C 204	3	30.0	17	18	US-10-877-623-10	Sequence 10, Appl
C 132	3	30.0	10	16	US-10-338-587A-14	Sequence 14, Appl	C 205	3	30.0	18	15	US-10-274-095-46	Sequence 46, Appl
C 133	3	30.0	10	16	US-10-338-587A-14	Sequence 14, Appl	C 206	3	30.0	18	15	US-10-274-095-46	Sequence 46, Appl
C 134	3	30.0	10	16	US-10-172-526-15	Sequence 15, Appl	C 207	3	30.0	18	15	US-10-279-061-3	Sequence 3, Appl
C 135	3	30.0	10	16	US-10-172-526-15	Sequence 15, Appl	C 208	3	30.0	18	15	US-10-279-061-3	Sequence 3, Appl
C 136	3	30.0	10	18	US-10-689-006-32	Sequence 32, Appl	C 209	3	30.0	18	17	US-10-666-022-24	Sequence 24, Appl
C 137	3	30.0	10	18	US-10-689-006-32	Sequence 32, Appl	C 210	3	30.0	18	17	US-10-666-022-24	Sequence 24, Appl
C 138	3	30.0	10	18	US-10-888-694-23	Sequence 23, Appl	C 211	3	30.0	19	9	US-09-816-763-19	Sequence 19, Appl
C 139	3	30.0	12	15	US-10-359-050-3	Sequence 3, Appl	C 212	3	30.0	19	9	US-09-816-763-19	Sequence 19, Appl
C 140	3	30.0	12	15	US-10-359-050-3	Sequence 3, Appl	C 213	3	30.0	19	9	US-09-816-763-20	Sequence 20, Appl
C 141	3	30.0	12	15	US-10-359-050-4	Sequence 4, Appl	C 214	3	30.0	19	9	US-09-816-763-20	Sequence 20, Appl
C 142	3	30.0	12	15	US-10-359-050-4	Sequence 4, Appl	C 215	3	30.0	19	14	US-10-087-956-43	Sequence 43, Appl
C 143	3	30.0	12	15	US-10-359-050-4	Sequence 4, Appl	C 216	3	30.0	19	14	US-10-087-956-43	Sequence 43, Appl
C 144	3	30.0	12	15	US-10-300-011-78	Sequence 78, Appl	C 217	3	30.0	19	14	US-10-087-956-43	Sequence 43, Appl
C 145	3	30.0	12	15	US-10-300-011-78	Sequence 78, Appl	C 218	3	30.0	19	14	US-10-087-956-43	Sequence 43, Appl
C 146	3	30.0	13	9	US-09-816-763-67	Sequence 67, Appl	C 219	3	30.0	19	17	US-10-666-022-25	Sequence 25, Appl
C 147	3	30.0	13	9	US-09-816-763-67	Sequence 67, Appl	C 220	3	30.0	19	17	US-10-666-022-25	Sequence 25, Appl
C 148	3	30.0	13	16	US-10-602-837-15	Sequence 15, Appl	C 221	3	30.0	19	17	US-10-666-022-35	Sequence 35, Appl
C 149	3	30.0	13	16	US-10-602-837-15	Sequence 15, Appl	C 222	3	30.0	19	17	US-10-666-022-35	Sequence 35, Appl
C 150	3	30.0	13	17	US-10-821-568-67	Sequence 67, Appl	C 223	3	30.0	19	17	US-10-636-065-209	Sequence 209, App
C 151	3	30.0	13	17	US-10-821-568-67	Sequence 67, Appl	C 224	3	30.0	19	17	US-10-636-065-209	Sequence 209, App
C 152	3	30.0	14	9	US-09-802-807-7	Sequence 7, Appl	C 225	3	30.0	19	17	US-10-836-065-211	Sequence 211, App
C 153	3	30.0	14	10	US-09-845-020A-8	Sequence 8, Appl	C 226	3	30.0	19	17	US-10-821-568-19	Sequence 19, Appl
C 154	3	30.0	14	10	US-09-845-020A-8	Sequence 8, Appl	C 227	3	30.0	19	17	US-10-821-568-19	Sequence 19, Appl
C 155	3	30.0	14	15	US-10-345-115-1	Sequence 1, Appl	C 228	3	30.0	19	17	US-10-821-568-20	Sequence 20, Appl
C 156	3	30.0	14	15	US-10-345-115-1	Sequence 1, Appl	C 229	3	30.0	19	17	US-10-821-568-20	Sequence 20, Appl
C 157	3	30.0	14	16	US-10-277-612-1	Sequence 1, Appl	C 230	3	30.0	19	18	US-10-898-106-43	Sequence 43, Appl
C 158	3	30.0	14	16	US-10-277-612-1	Sequence 1, Appl	C 231	3	30.0	20	9	US-09-303-510-29	Sequence 29, Appl

C 232	3	30.0	20	9	US-09-303-510-29	Sequence 29, Appl	305	3	30.0	23	9	US-09-971-309-48	Sequence 48, Appl
C 233	3	30.0	20	14	US-10-243-501-4	Sequence 4, Appl	C 306	3	30.0	23	9	US-09-971-309-48	Sequence 48, Appl
C 234	3	30.0	20	14	US-10-243-501-4	Sequence 4, Appl	C 307	3	30.0	23	10	US-09-468-147-148	Sequence 148, App
C 235	3	30.0	20	14	US-10-243-351-3	Sequence 3, Appl	C 308	3	30.0	23	10	US-09-468-147-148	Sequence 148, App
C 236	3	30.0	20	14	US-10-243-351-3	Sequence 3, Appl	C 309	3	30.0	23	10	US-09-468-147-148	Sequence 148, App
C 237	3	30.0	20	15	US-10-273-051-19	Sequence 19, Appl	C 310	3	30.0	23	10	US-09-468-147-148	Sequence 148, App
C 238	3	30.0	20	15	US-10-273-051-19	Sequence 19, Appl	C 311	3	30.0	23	15	US-10-258-107-15	Sequence 15, Appl
C 239	3	30.0	20	15	US-10-404-300A-30	Sequence 30, Appl	C 312	3	30.0	23	15	US-10-258-107-15	Sequence 15, Appl
C 240	3	30.0	20	15	US-10-404-300A-30	Sequence 30, Appl	C 313	3	30.0	23	15	US-10-258-107-15	Sequence 15, Appl
C 241	3	30.0	20	15	US-10-129-518-19	Sequence 19, Appl	C 314	3	30.0	23	15	US-10-319-745-148	Sequence 148, App
C 242	3	30.0	20	15	US-10-129-518-19	Sequence 19, Appl	C 315	3	30.0	23	15	US-10-319-745-148	Sequence 148, App
C 243	3	30.0	20	16	US-10-338-110-54	Sequence 54, Appl	C 316	3	30.0	23	15	US-10-319-745-255	Sequence 255, App
C 244	3	30.0	20	16	US-10-338-110-54	Sequence 54, Appl	C 317	3	30.0	23	15	US-10-319-745-255	Sequence 255, App
C 245	3	30.0	20	17	US-10-666-022-36	Sequence 26, Appl	C 318	3	30.0	23	16	US-10-362-091-21	Sequence 21, Appl
C 246	3	30.0	20	17	US-10-666-022-36	Sequence 26, Appl	C 319	3	30.0	23	16	US-10-362-091-21	Sequence 21, Appl
C 247	3	30.0	20	17	US-10-666-022-36	Sequence 26, Appl	C 320	3	30.0	23	17	US-10-666-022-29	Sequence 29, Appl
C 248	3	30.0	20	17	US-10-666-022-36	Sequence 26, Appl	C 321	3	30.0	23	17	US-10-666-022-29	Sequence 29, Appl
C 249	3	30.0	20	17	US-10-666-022-46	Sequence 36, Appl	C 322	3	30.0	23	17	US-10-666-022-39	Sequence 39, Appl
C 250	3	30.0	20	17	US-10-666-022-46	Sequence 36, Appl	C 323	3	30.0	23	17	US-10-666-022-39	Sequence 39, Appl
C 251	3	30.0	20	17	US-10-666-022-46	Sequence 36, Appl	C 324	3	30.0	23	17	US-10-666-022-49	Sequence 49, Appl
C 252	3	30.0	20	17	US-10-666-022-101	Sequence 101, App	C 325	3	30.0	23	17	US-10-666-022-49	Sequence 49, Appl
C 253	3	30.0	20	17	US-10-666-022-101	Sequence 101, App	C 326	3	30.0	23	17	US-10-666-022-59	Sequence 59, Appl
C 254	3	30.0	20	17	US-10-641-665A-1	Sequence 1, Appl	C 327	3	30.0	23	17	US-10-666-022-59	Sequence 59, Appl
C 255	3	30.0	20	17	US-10-641-665A-1	Sequence 1, Appl	C 328	3	30.0	23	17	US-10-666-022-69	Sequence 69, Appl
C 256	3	30.0	20	17	US-10-641-665A-3	Sequence 3, Appl	C 329	3	30.0	23	17	US-10-666-022-79	Sequence 79, Appl
C 257	3	30.0	20	17	US-10-729-172-36	Sequence 36, Appl	C 330	3	30.0	23	17	US-10-666-022-79	Sequence 79, Appl
C 258	3	30.0	20	17	US-10-729-172-36	Sequence 36, Appl	C 331	3	30.0	23	17	US-10-666-022-104	Sequence 104, App
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C 261	3	30.0	21	10	US-09-928-267-3	Sequence 3, Appl	C 334	3	30.0	23	17	US-10-666-022-114	Sequence 114, App
C 262	3	30.0	21	10	US-09-928-267-3	Sequence 3, Appl	C 335	3	30.0	23	17	US-10-666-022-124	Sequence 124, App
C 263	3	30.0	21	15	US-10-377-133-20	Sequence 20, Appl	C 336	3	30.0	23	17	US-10-666-022-124	Sequence 124, App
C 264	3	30.0	21	15	US-10-377-133-20	Sequence 20, Appl	C 337	3	30.0	23	17	US-10-666-022-134	Sequence 134, App
C 265	3	30.0	21	15	US-10-377-133-28	Sequence 28, Appl	C 338	3	30.0	23	17	US-10-666-022-134	Sequence 134, App
C 266	3	30.0	21	15	US-10-377-133-28	Sequence 28, Appl	C 339	3	30.0	23	17	US-10-637-544-11	Sequence 11, Appl
C 267	3	30.0	21	15	US-10-377-133-30	Sequence 30, Appl	C 340	3	30.0	23	17	US-10-637-544-11	Sequence 11, Appl
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C 269	3	30.0	21	15	US-10-418-182-99	Sequence 99, Appl	C 342	3	30.0	24	9	US-09-785-632A-82	Sequence 82, Appl
C 270	3	30.0	21	15	US-10-418-182-99	Sequence 99, Appl	C 343	3	30.0	24	15	US-10-278-087A-15	Sequence 15, Appl
C 271	3	30.0	21	15	US-10-418-182-311	Sequence 311, App	C 344	3	30.0	24	15	US-10-278-087A-15	Sequence 15, Appl
C 272	3	30.0	21	15	US-10-418-182-311	Sequence 311, App	C 345	3	30.0	24	15	US-10-278-087A-15	Sequence 15, Appl
C 273	3	30.0	21	16	US-10-407-897-48	Sequence 48, Appl	C 346	3	30.0	24	15	US-10-080-263C-7	Sequence 7, Appl
C 274	3	30.0	21	16	US-10-407-897-48	Sequence 48, Appl	C 347	3	30.0	24	15	US-10-080-263C-7	Sequence 7, Appl
C 275	3	30.0	21	17	US-10-666-022-27	Sequence 27, Appl	C 348	3	30.0	24	15	US-10-223-765-82	Sequence 82, Appl
C 276	3	30.0	21	17	US-10-666-022-27	Sequence 27, Appl	C 349	3	30.0	24	15	US-10-223-765-82	Sequence 82, Appl
C 277	3	30.0	21	17	US-10-666-022-37	Sequence 37, Appl	C 350	3	30.0	24	17	US-10-666-022-30	Sequence 30, Appl
C 278	3	30.0	21	17	US-10-666-022-37	Sequence 37, Appl	C 351	3	30.0	24	17	US-10-666-022-30	Sequence 30, Appl
C 279	3	30.0	21	17	US-10-666-022-47	Sequence 47, Appl	C 352	3	30.0	24	17	US-10-666-022-40	Sequence 40, Appl
C 280	3	30.0	21	17	US-10-666-022-47	Sequence 47, Appl	C 353	3	30.0	24	17	US-10-666-022-50	Sequence 50, Appl
C 281	3	30.0	21	17	US-10-666-022-57	Sequence 57, Appl	C 354	3	30.0	24	17	US-10-666-022-50	Sequence 50, Appl
C 282	3	30.0	21	17	US-10-666-022-57	Sequence 57, Appl	C 355	3	30.0	24	17	US-10-666-022-60	Sequence 60, Appl
C 283	3	30.0	21	17	US-10-666-022-102	Sequence 102, App	C 356	3	30.0	24	17	US-10-666-022-60	Sequence 60, Appl
C 284	3	30.0	21	17	US-10-666-022-102	Sequence 102, App	C 357	3	30.0	24	17	US-10-666-022-70	Sequence 70, Appl
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C 286	3	30.0	21	17	US-10-666-022-112	Sequence 112, App	C 359	3	30.0	24	17	US-10-666-022-80	Sequence 80, Appl
C 287	3	30.0	21	17	US-10-433-244-12	Sequence 12, Appl	C 360	3	30.0	24	17	US-10-666-022-80	Sequence 80, Appl
C 288	3	30.0	21	17	US-10-433-244-12	Sequence 12, Appl	C 361	3	30.0	24	17	US-10-666-022-90	Sequence 90, Appl
C 289	3	30.0	21	17	US-10-666-022-28	Sequence 28, Appl	C 362	3	30.0	24	17	US-10-666-022-90	Sequence 90, Appl
C 290	3	30.0	22	17	US-10-666-022-28	Sequence 28, Appl	C 363	3	30.0	24	17	US-10-666-022-105	Sequence 105, App
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C 292	3	30.0	22	17	US-10-666-022-38	Sequence 38, Appl	C 365	3	30.0	24	17	US-10-666-022-115	Sequence 115, App
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c 530	28	18	US-10-795-667-11	Sequence 11, Appl	c 603	3	30.0	32	15	US-10-104-706-2	Sequence 2, Appl
c 531	28	18	US-10-257-047-53	Sequence 53, Appl	c 604	3	30.0	32	15	US-10-104-706-2	Sequence 2, Appl
c 532	28	18	US-10-257-047-53	Sequence 53, Appl	c 605	3	30.0	32	16	US-10-299-636-31	Sequence 31, Appl
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c 541	29	17	US-10-666-022-65	Sequence 65, Appl	c 614	3	30.0	32	17	US-10-666-022-173	Sequence 173, App
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c 543	29	17	US-10-666-022-75	Sequence 75, Appl	c 616	3	30.0	32	18	US-10-795-667-15	Sequence 15, Appl
c 544	29	17	US-10-666-022-75	Sequence 75, Appl	c 617	3	30.0	33	9	US-09-991-119-11	GENERAL INFORMA
c 545	29	17	US-10-666-022-85	Sequence 85, Appl	c 618	3	30.0	33	9	US-09-991-119-11	GENERAL INFORMA
c 546	29	17	US-10-666-022-85	Sequence 85, Appl	c 619	3	30.0	33	15	US-10-126-845-36	Sequence 36, Appl
c 547	29	17	US-10-666-022-95	Sequence 95, Appl	c 620	3	30.0	33	15	US-10-126-845-36	Sequence 36, Appl
c 548	29	17	US-10-666-022-95	Sequence 95, Appl	c 621	3	30.0	33	17	US-10-666-022-164	Sequence 164, App
c 549	29	17	US-10-666-022-120	Sequence 120, App	c 622	3	30.0	33	17	US-10-666-022-164	Sequence 164, App
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c 554	29	17	US-10-666-022-140	Sequence 140, App	c 627	3	30.0	33	17	US-10-758-622-11	GENERAL INFORMA
c 555	29	17	US-10-666-022-150	Sequence 150, App	c 628	3	30.0	33	17	US-10-758-622-11	GENERAL INFORMA
c 556	29	17	US-10-666-022-150	Sequence 150, App	c 629	3	30.0	33	18	US-10-795-667-16	Sequence 16, Appl
c 557	29	17	US-10-666-022-160	Sequence 160, App	c 630	3	30.0	33	18	US-10-795-667-16	Sequence 16, Appl
c 558	29	17	US-10-666-022-160	Sequence 160, App	c 631	3	30.0	34	9	US-09-784-982-13	Sequence 13, Appl
c 559	29	17	US-10-666-022-170	Sequence 170, App	c 632	3	30.0	34	9	US-09-784-982-13	Sequence 13, Appl
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c 565	30	17	US-10-666-022-86	Sequence 86, Appl	c 638	3	30.0	34	18	US-10-795-667-17	Sequence 17, Appl
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c 596	31	17	US-10-666-022-152	Sequence 152, App	c 669	3	30.0	39	9	US-09-881-823-26	Sequence 26, Appl

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c 715	3	30.0	3	42	US-08-934-000-23	Sequence 23, Appl	c 788	15	US-10-149-835C-6	Sequence 6, Appl
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c 839	3	30.0	77	17	US-10-693-057-451	Sequence 451, App	c 912	3	30.0	90	16	US-10-296-734-234	Sequence 234, App
c 840	3	30.0	77	17	US-10-693-057-451	Sequence 451, App	c 913	3	30.0	90	16	US-10-296-734-236	Sequence 236, App
c 841	3	30.0	77	17	US-10-693-057-462	Sequence 462, App	c 914	3	30.0	90	16	US-10-296-734-236	Sequence 236, App
c 842	3	30.0	77	17	US-10-693-057-462	Sequence 462, App	c 915	3	30.0	90	16	US-10-296-734-256	Sequence 256, App
c 843	3	30.0	77	17	US-10-693-057-492	Sequence 492, App	c 916	3	30.0	90	16	US-10-296-734-256	Sequence 256, App
c 844	3	30.0	77	17	US-10-693-057-492	Sequence 492, App	c 917	3	30.0	91	13	US-10-092-140-5	Sequence 5, Appli
c 845	3	30.0	77	17	US-10-693-057-503	Sequence 503, App	c 918	3	30.0	91	13	US-10-092-140-5	Sequence 5, Appli
c 846	3	30.0	77	17	US-10-693-057-503	Sequence 503, App	c 919	3	30.0	95	14	US-10-123-155-62	Sequence 62, Appl
c 847	3	30.0	79	17	US-10-693-057-440	Sequence 440, App	c 920	3	30.0	95	14	US-10-123-155-62	Sequence 62, Appl
c 848	3	30.0	79	17	US-10-693-057-440	Sequence 440, App	c 921	3	30.0	95	15	US-10-146-731-62	Sequence 62, Appl
c 849	3	30.0	79	17	US-10-693-057-481	Sequence 481, App	c 922	3	30.0	95	15	US-10-146-731-62	Sequence 62, Appl
c 850	3	30.0	79	17	US-10-693-057-481	Sequence 481, App	c 923	3	30.0	95	15	US-10-140-472-62	Sequence 62, Appl
c 851	3	30.0	81	14	US-10-112-612-34	Sequence 34, Appl	c 924	3	30.0	95	15	US-10-140-472-62	Sequence 62, Appl
c 852	3	30.0	81	14	US-10-112-612-34	Sequence 34, Appl	c 925	3	30.0	95	15	US-10-141-761-62	Sequence 62, Appl
c 853	3	30.0	81	15	US-10-112-691-34	Sequence 34, Appl	c 926	3	30.0	95	15	US-10-141-761-62	Sequence 62, Appl
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c 855	3	30.0	81	15	US-10-423-495-36	Sequence 36, Appl	c 928	3	30.0	95	15	US-10-142-885-62	Sequence 62, Appl
c 856	3	30.0	81	15	US-10-423-495-36	Sequence 36, Appl	c 929	3	30.0	95	15	US-10-158-790-62	Sequence 62, Appl
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c 859	3	30.0	82	17	US-10-693-057-480	Sequence 480, App	c 932	3	30.0	95	15	US-10-137-871-62	Sequence 62, Appl
c 860	3	30.0	82	17	US-10-693-057-480	Sequence 480, App	c 933	3	30.0	95	15	US-10-140-923-62	Sequence 62, Appl
c 861	3	30.0	83	17	US-10-693-057-452	Sequence 452, App	c 934	3	30.0	95	15	US-10-140-923-62	Sequence 62, Appl
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c 863	3	30.0	83	17	US-10-693-057-463	Sequence 463, App	c 936	3	30.0	95	15	US-10-141-756-62	Sequence 62, Appl
c 864	3	30.0	83	17	US-10-693-057-493	Sequence 493, App	c 937	3	30.0	95	15	US-10-141-759-62	Sequence 62, Appl
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c 866	3	30.0	83	17	US-10-693-057-493	Sequence 493, App	c 939	3	30.0	95	15	US-10-140-805-62	Sequence 62, Appl
c 867	3	30.0	83	17	US-10-693-057-504	Sequence 504, App	c 940	3	30.0	95	15	US-10-140-805-62	Sequence 62, Appl
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c 869	3	30.0	84	14	US-10-184-644-186	Sequence 186, App	c 942	3	30.0	95	15	US-10-140-864-62	Sequence 62, Appl
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c 872	3	30.0	84	14	US-10-184-644-186	Sequence 186, App	c 945	3	30.0	97	10	US-09-849-928-272	Sequence 272, App
c 873	3	30.0	84	14	US-10-184-644-186	Sequence 186, App	c 946	3	30.0	97	10	US-09-849-928-272	Sequence 272, App
c 874	3	30.0	84	14	US-10-184-634-186	Sequence 186, App	c 947	3	30.0	97	14	US-10-066-960-272	Sequence 272, App
c 875	3	30.0	84	14	US-10-133-128-229	Sequence 229, App	c 948	3	30.0	97	14	US-10-066-960-272	Sequence 272, App
c 876	3	30.0	84	14	US-10-133-128-229	Sequence 229, App	c 949	3	30.0	97	16	US-10-409-627-272	Sequence 272, App
c 877	3	30.0	84	14	US-10-133-128-230	Sequence 230, App	c 950	3	30.0	97	16	US-10-409-627-272	Sequence 272, App
c 878	3	30.0	84	14	US-10-133-128-230	Sequence 230, App	c 951	3	30.0	97	16	US-10-705-300-272	Sequence 272, App
c 879	3	30.0	84	15	US-10-289-660-229	Sequence 229, App	c 952	3	30.0	97	16	US-10-705-300-272	Sequence 272, App
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c 883	3	30.0	84	15	US-10-112-691-61	Sequence 61, Appl	c 956	3	30.0	100	14	US-10-184-634-526	Sequence 526, App
c 884	3	30.0	84	15	US-10-112-691-61	Sequence 61, Appl	c 957	2	20.0	4	9	US-09-760-506-5	Sequence 5, Appli
c 885	3	30.0	84	15	US-10-112-691-61	Sequence 61, Appl	c 958	2	20.0	4	9	US-09-760-506-5	Sequence 5, Appli
c 886	3	30.0	84	15	US-10-063-685-44	Sequence 44, Appl	c 959	2	20.0	4	17	US-10-293-252C-2	Sequence 2, Appli
c 887	3	30.0	84	15	US-10-063-685-44	Sequence 44, Appl	c 960	2	20.0	4	17	US-10-293-252C-2	Sequence 2, Appli
c 888	3	30.0	84	15	US-10-423-495-58	Sequence 58, Appl	c 961	2	20.0	4	17	US-10-293-252C-6	Sequence 6, Appli

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c 989      2 20.0      6 9 US-09-920-313-87
c 990      2 20.0      6 10 US-09-798-883B-55
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c 992      2 20.0      6 10 US-09-882-274-5
c 993      2 20.0      6 10 US-09-882-274-5
c 994      2 20.0      6 10 US-09-326-885-55
c 995      2 20.0      6 10 US-09-326-885-55
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c 999      2 20.0      6 13 US-10-117-641-10
c1000     2 20.0      6 13 US-10-117-641-10

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Sequence 2, Appli
Sequence 2, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 8, Appli
Sequence 8, Appli
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Sequence 55, Appl
Sequence 55, Appl
Sequence 87, Appl
Sequence 87, Appl
Sequence 10, Appl

SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-813-824A-3

Query Match      100.0%; Score 10; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRRCWGYYY 10
Db      1 RRRCWGYYY 10

RESULT 2
US-09-813-824A-3/c
; Sequence 3, Application US/09813824A
; Patent No. US20020164595A1
; GENERAL INFORMATION:
; APPLICANT: Vogelstein, Bert
; Kinzler, Kenneth
; Sherman, Michael
; TITLE OF INVENTION: SEQUENCE SPECIFIC DNA BINDING
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Banner & Witcoff
; STREET: 1001 G Street, NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/813,824A
; FILING DATE: 22-Mar-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/860,758
; FILING DATE: 31-Mar-1992
; APPLICATION NUMBER: 07/715,182
; FILING DATE: 14-JUN-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Kagan, Sarah A
; REGISTRATION NUMBER: 32141
; REFERENCE/DOCKET NUMBER: 01107.47071
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-508-9100
; TELEFAX: 202-508-9299
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid

FILING DATE: 31-MAR-1992
APPLICATION NUMBER: 07/715,182
ATTORNEY/AGENT INFORMATION:
NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32141
REFERENCE/DOCKET NUMBER: 01107.47071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9299
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid
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;
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-813-824A-3

Query Match 100.0%; Score 10; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10
||| |||||
Db 10 RRRCWGYYY 1

RESULT 3
US-09-928-385B-24
; Sequence 24, Application US/09928385B
; Publication No. US20030049625A1
; GENERAL INFORMATION:
; APPLICANT: Heyduk, Tomasz
; TITLE OF INVENTION: A Rapid and Sensitive Proximity-Based Assay for the Detection
; FILE REFERENCE: 16153-7963
; CURRENT APPLICATION NUMBER: US/09/928,385B
; CURRENT FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY:
; FEATURE:
; LOCATION:
; OTHER INFORMATION: These sequences were chemically synthesized,
; OTHER INFORMATION: but may also be created via recombinant methods.
US-09-928-385B-24

Query Match 100.0%; Score 10; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10
||| |||||
Db 1 RRRCWGYYY 10

RESULT 4
US-09-928-385B-24/c
; Sequence 24, Application US/09928385B
; Publication No. US20030049625A1
; GENERAL INFORMATION:
; APPLICANT: Heyduk, Tomasz
; TITLE OF INVENTION: A Rapid and Sensitive Proximity-Based Assay for the Detection
; FILE REFERENCE: 16153-7963
; CURRENT APPLICATION NUMBER: US/09/928,385B
; CURRENT FILING DATE: 2002-01-14
; NUMBER OF SEQ ID NOS: 24
; SEQ ID NO 24
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: These sequences were chemically synthesized,
; OTHER INFORMATION: but may also be created via recombinant methods.
US-09-928-385B-24

Query Match 100.0%; Score 10; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10
||| |||||
Db 10 RRRCWGYYY 1

RESULT 5
US-09-798-883B-57
; Sequence 57, Application US/09798883B
; Publication No. US20030159159A1
; GENERAL INFORMATION:
; APPLICANT: LINNIK, Matthew
; APPLICANT: RACKE, Margaret
; APPLICANT: KRAKOWSKY, Joan
; APPLICANT: SUBRAMANIAM, Arun
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and Exon 3 Promoters
; FILE REFERENCE: HMR2002C US DIV
; CURRENT APPLICATION NUMBER: US/09/798,883B
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Binding Motif in Human Nerve Growth Factor Exon 1 and Exon 3 Promoters
; OTHER INFORMATION: Promoter
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: r=g or a
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: y=c or t
US-09-798-883B-57

Query Match 100.0%; Score 10; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRCWGYYY 10
||| |||||
Db 1 RRRCWGYYY 10

RESULT 6
US-09-798-883B-57/c
; Sequence 57, Application US/09798883B
; Publication No. US20030159159A1
; GENERAL INFORMATION:
; APPLICANT: LINNIK, Matthew
; APPLICANT: RACKE, Margaret
; APPLICANT: KRAKOWSKY, Joan
; APPLICANT: SUBRAMANIAM, Arun
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and Exon 3 Promoters
; FILE REFERENCE: HMR2002C US DIV
; CURRENT APPLICATION NUMBER: US/09/798,883B
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 57
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Binding Motif in Human Nerve Growth Factor Exon 1 and Exon 3 Promoters
; OTHER INFORMATION: Promoter
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: r=g or a
; FEATURE:
US-09-798-883B-57

Query Match 100.0%; Score 10; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

NAME/KEY: misc feature
 OTHER INFORMATION: w=a or t
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: y=c or t
 US-09-798-883B-57

Query Match 100.0%; Score 10; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10
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 DB 10 RRRCWGYYY 1

RESULT 7

US-09-326-885-57
 ; Sequence 57, Application US/09326885
 ; Publication No. US20030192065A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Linnik, Matthew D
 ; Racke, Margaret M
 ; Krakowsky, Joan M
 ; Subramaniam, Arun
 ; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and
 ; Exon 3 Promoters

NUMBER OF SEQUENCES: 84
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Hoechst Marion Roussel, Inc.
 STREET: 2110 East Galbraith Road, P.O. Box 156300
 CITY: Cincinnati
 STATE: Ohio
 COUNTRY: United States of America
 ZIP: 45215-6300

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/326,885
 FILING DATE: 07-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/020,179
 FILING DATE: <Unknown>

APPLICATION NUMBER: US 60/038,212
 FILING DATE: 06-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Payne, T. Helen
 REGISTRATION NUMBER: 36,889

REFERENCE/DOCKET NUMBER: HMR2002A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 513 948-7183
 TELEFAX: 513 948-7961/4681
 TELEX: 214320

INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 57:
 US-09-326-885-57

Query Match 100.0%; Score 10; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10
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Db 1 RRRCWGYYY 10

RESULT 8

US-09-326-885-57/c
 ; Sequence 57, Application US/09326885
 ; Publication No. US20030192065A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Linnik, Matthew D
 ; Racke, Margaret M
 ; Krakowsky, Joan M
 ; Subramaniam, Arun

TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and
 ; Exon 3 Promoters
 ; NUMBER OF SEQUENCES: 84
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Hoechst Marion Roussel, Inc.
 ; STREET: 2110 East Galbraith Road, P.O. Box 156300
 ; CITY: Cincinnati
 ; STATE: Ohio
 ; COUNTRY: United States of America
 ; ZIP: 45215-6300

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/326,885
 FILING DATE: 07-Jun-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/020,179
 FILING DATE: <Unknown>

APPLICATION NUMBER: US 60/038,212
 FILING DATE: 06-FEB-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Payne, T. Helen
 REGISTRATION NUMBER: 36,889

REFERENCE/DOCKET NUMBER: HMR2002A
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 513 948-7183
 TELEFAX: 513 948-7961/4681
 TELEX: 214320

INFORMATION FOR SEQ ID NO: 57:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 10 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: unknown
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 57:
 US-09-326-885-57

Query Match 100.0%; Score 10; DB 10; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCWGYYY 10
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 DB 10 RRRCWGYYY 1

RESULT 9

US-10-464-996-5
 ; Sequence 5, Application US/10464996
 ; Publication No. US20040101915A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Devereaux, Quinn L.
 ; APPLICANT: Wagner, Klaus W.
 ; APPLICANT: Hampton, Garret M.
 ; APPLICANT: IRM LLC
 ; TITLE OF INVENTION: Diagnosis and Treatment of Chemoresistant Tumors

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; FILE REFERENCE: 021288-001220US
; CURRENT APPLICATION NUMBER: US/10/464,996
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/390,256
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/456,585
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p53 consensus
; OTHER INFORMATION: element
US-10-464-996-5

Query Match          100.0%; Score 10; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 1 RRRRCWGGYY 10

RESULT 10
US-10-464-996-5/c
; Sequence 5, Application US/10464996
; Publication No. US20040101915A1
; GENERAL INFORMATION:
; APPLICANT: Deveraux, Quinn L.
; APPLICANT: Wagner, Klaus W.
; APPLICANT: Hampton, Garret M.
; APPLICANT: IRM LLC
; TITLE OF INVENTION: Diagnosis and Treatment of Chemoresistant Tumors
; FILE REFERENCE: 021288-001220US
; CURRENT APPLICATION NUMBER: US/10/464,996
; CURRENT FILING DATE: 2003-06-18
; PRIOR APPLICATION NUMBER: US 60/390,256
; PRIOR FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: US 60/456,585
; PRIOR FILING DATE: 2003-03-21
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:p53 consensus
; OTHER INFORMATION: element
US-10-464-996-5

Query Match          100.0%; Score 10; DB 17; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 10 RRRRCWGGYY 1

RESULT 11
US-10-795-933-21
; Sequence 21, Application US/10795933
; Publication No. US20040259126A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
```

```
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/10/795,933
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/08/260,190
; PRIOR FILING DATE: 1994-06-15
; PRIOR APPLICATION NUMBER: 08/177,093
; PRIOR FILING DATE: 1993-12-30
; PRIOR APPLICATION NUMBER: 07/964,589
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: PV-709-92
; PRIOR FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(10)
US-10-795-933-21

Query Match          100.0%; Score 10; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 1 RRRRCWGGYY 10

RESULT 12
US-10-795-933-21/c
; Sequence 21, Application US/10795933
; Publication No. US20040259126A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021-2
; CURRENT APPLICATION NUMBER: US/10/795,933
; CURRENT FILING DATE: 2004-03-08
; PRIOR APPLICATION NUMBER: US/08/260,190
; PRIOR FILING DATE: 1994-06-15
; PRIOR APPLICATION NUMBER: 08/177,093
; PRIOR FILING DATE: 1993-12-30
; PRIOR APPLICATION NUMBER: 07/964,589
; PRIOR FILING DATE: 1992-10-21
; PRIOR APPLICATION NUMBER: PV-709-92
; PRIOR FILING DATE: 1992-03-11
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)..(10)
US-10-795-933-21

Query Match          100.0%; Score 10; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
Db 10 RRRRCWGGYY 1

RESULT 13
US-10-450-436-26
```

```
; Sequence 26, Application US/10450436
; Publication No. US20040077832A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jian
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: JFV1 induces rapid apoptosis
; FILE REFERENCE: 01107.00062
; CURRENT APPLICATION NUMBER: US/10/450,436
; CURRENT FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-436-26

Query Match      100.0%; Score 10; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRCWGWGYYY 10
      |||||
Db      10 RRCWGWGYYY 19

RESULT 14
US-10-450-436-26/c
; Sequence 26, Application US/10450436
; Publication No. US20040077832A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Jian
; APPLICANT: Kinzler, Kenneth
; APPLICANT: Vogelstein, Bert
; TITLE OF INVENTION: JFV1 induces rapid apoptosis
; FILE REFERENCE: 01107.00062
; CURRENT APPLICATION NUMBER: US/10/450,436
; CURRENT FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-450-436-26

Query Match      100.0%; Score 10; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRCWGWGYYY 10
      |||||
Db      10 RRCWGWGYYY 19

RESULT 15
US-09-939-581A-6
; Sequence 6, Application US/09939581A
; Patent No. US20020102245A1
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; CURRENT APPLICATION NUMBER: US/09/939,581A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/210,748
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-939-581A-6

Query Match      100.0%; Score 10; DB 16; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRCWGWGYYY 10
      |||||
Db      19 RRCWGWGYYY 10

RESULT 16
US-09-939-581A-6/c
; Sequence 6, Application US/09939581A
; Patent No. US20020102245A1
; GENERAL INFORMATION:
; APPLICANT: Hermeking, Heiko
; APPLICANT: Vogelstein, Bert
; APPLICANT: Kinzler, Kenneth
; TITLE OF INVENTION: 14-3-3 SIGMA ARREST THE CELL CYCLE
; CURRENT APPLICATION NUMBER: US/09/939,581A
; CURRENT FILING DATE: 2001-08-28
; PRIOR APPLICATION NUMBER: 09/210,748
; PRIOR FILING DATE: 1998-12-15
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-939-581A-6

Query Match      100.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRCWGWGYYY 10
      |||||
Db      1 RRCWGWGYYY 10

RESULT 17
US-09-816-763-92
; Sequence 92, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor P53
US-09-816-763-92

Query Match      100.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
```


Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
|||||
Db 1 RRCWGWYYY 10

RESULT 18
US-10-816-763-92/c
; Sequence 92, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor P53
US-09-816-763-92

Query Match 100.0%; Score 10; DB 9; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
|||||
Db 20 RRCWGWYYY 11

RESULT 19
US-10-821-568-92
; Sequence 92, Application US/10821568
; Patent No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor P53
US-10-821-568-92

Query Match 100.0%; Score 10; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
|||||
Db 1 RRCWGWYYY 10

RESULT 20
US-10-821-568-92/c
; Sequence 92, Application US/10821568
; Patent No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor P53
US-10-821-568-92

Query Match 100.0%; Score 10; DB 17; Length 20;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
|||||
Db 20 RRCWGWYYY 11

RESULT 21
US-09-816-763-133
; Sequence 133, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)-(21)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-133

Query Match 100.0%; Score 10; DB 9; Length 21;

```
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
    |||||
Db 12 RRCWGWYYY 21

RESULT 22
US-09-816-763-133/c
; Sequence 133, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(21)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-133

Query Match 100.0%; Score 10; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
    |||||
Db 21 RRCWGWYYY 12

RESULT 23
US-10-821-568-133
; Sequence 133, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(21)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-133

Query Match 100.0%; Score 10; DB 9; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
    |||||
Db 21 RRCWGWYYY 12

RESULT 24
US-10-821-568-133/c
; Sequence 133, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(21)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-133

Query Match 100.0%; Score 10; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
    |||||
Db 12 RRCWGWYYY 21

RESULT 25
US-09-816-763-134
; Sequence 134, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(21)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-133

Query Match 100.0%; Score 10; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
    |||||
Db 21 RRCWGWYYY 12

RESULT 26
US-09-816-763-134
; Sequence 134, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(21)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-133
```

```
; NAME/KEY: misc_feature
; LOCATION: (1)...(21)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-133

Query Match 100.0%; Score 10; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
    |||||
Db 12 RRCWGWYYY 21

RESULT 24
US-10-821-568-133/c
; Sequence 133, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(21)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-133

Query Match 100.0%; Score 10; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
    |||||
Db 21 RRCWGWYYY 12

RESULT 25
US-09-816-763-134
; Sequence 134, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(21)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-133

Query Match 100.0%; Score 10; DB 17; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCWGWYYY 10
    |||||
Db 21 RRCWGWYYY 12

RESULT 26
US-09-816-763-134
; Sequence 134, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 133
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(21)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-133
```

```
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc.feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-134

Query Match      100.0%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCCWGGYY 10
   |||||
Db 13 RRRCCWGGYY 22

RESULT 26
US-09-816-763-134/c
; Sequence 134, Application US/09816763
; Publication No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc.feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-134

Query Match      100.0%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCCWGGYY 10
   |||||
Db 22 RRRCCWGGYY 13

RESULT 27
US-10-821-568-134
; Sequence 134, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/10/821,568
; PRIOR FILING DATE: 2004-04-08
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc.feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-134

Query Match      100.0%; Score 10; DB 9; Length 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCCWGGYY 10
   |||||
Db 22 RRRCCWGGYY 13
```

```
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc.feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-134

Query Match      100.0%; Score 10; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCCWGGYY 10
   |||||
Db 13 RRRCCWGGYY 22

RESULT 28
US-10-821-568-134/c
; Sequence 134, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 134
; LENGTH: 22
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc.feature
; LOCATION: (1)...(22)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-134

Query Match      100.0%; Score 10; DB 17; Length 22;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRCCWGGYY 10
   |||||
Db 22 RRRCCWGGYY 13

RESULT 29
US-09-816-763-135
; Sequence 135, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
```

```

; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-135

```

```

Query Match      100.0%; Score 10; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RRRRCWGGYY 10
    |||||
Db 14 RRRRCWGGYY 23

```

```

RESULT 30
US-09-816-763-135/c
; Sequence 135, Application US/09816763
; Patent No. US2002011081A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-135

```

```

Query Match      100.0%; Score 10; DB 9; Length 23;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RRRRCWGGYY 10
    |||||
Db 23 RRRRCWGGYY 14

```

```

RESULT 31
US-10-821-568-135
; Sequence 135, Application US/10821568

```

```

; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-135

```

```

Query Match      100.0%; Score 10; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 RRRRCWGGYY 10
    |||||
Db 14 RRRRCWGGYY 23

```

```

RESULT 32
US-10-821-568-135/c
; Sequence 135, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(23)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-135

```

```

Query Match      100.0%; Score 10; DB 17; Length 23;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
Qy 1 RRCWGWYYY 10
    |||||
Db 23 RRCWGWYYY 14

RESULT 33
US-09-816-763-136
; Sequence 136, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)...(24)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-136

Query Match 100.0%; Score 10; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 15 RRCWGWYYY 24

RESULT 34
US-09-816-763-136/c
; Sequence 136, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)...(24)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-136

Query Match 100.0%; Score 10; DB 9; Length 24;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 15 RRCWGWYYY 24

RESULT 35
US-10-821-568-136
; Sequence 136, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(24)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-136

Query Match 100.0%; Score 10; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
    |||||
Db 15 RRCWGWYYY 24

RESULT 36
US-10-821-568-136/c
; Sequence 136, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 136
; LENGTH: 24
; TYPE: DNA
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(24)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-136

Query Match      100.0%; Score 10; DB 17; Length 24;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRCWGGYY 10
Db 24 RRCRCWGGYY 15

RESULT 37
US-09-816-763-137
; Sequence 137, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-137

Query Match      100.0%; Score 10; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRCWGGYY 10
Db 16 RRCRCWGGYY 25

RESULT 38
US-09-816-763-137/c
; Sequence 137, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: p53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-137

Query Match      100.0%; Score 10; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRCWGGYY 10
Db 25 RRCRCWGGYY 16

RESULT 39
US-10-821-568-137
; Sequence 137, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DVI
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-137

Query Match      100.0%; Score 10; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRCRCWGGYY 10
Db 16 RRCRCWGGYY 25

RESULT 40
US-10-821-568-137/c
; Sequence 137, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
```

```
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 137
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
; LOCATION: (1)...(25)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-137

Query Match      100.0%; Score 10; DB 17; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      25 RRRCWGYY 16

RESULT 41
US-09-816-763-138
; Sequence 138, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: DETECTION AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)...(26)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-138

Query Match      100.0%; Score 10; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      17 RRRCWGYY 26

RESULT 42
US-09-816-763-138/c
; Sequence 138, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)...(26)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-138

Query Match      100.0%; Score 10; DB 9; Length 26;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      26 RRRCWGYY 17

RESULT 43
US-10-821-568-138
; Sequence 138, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(26)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-138

Query Match      100.0%; Score 10; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      17 RRRCWGYY 26
```

```
RESULT 44
US-10-821-568-138/c
; Sequence 138, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 138
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)..(26)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-138

Query Match      100.0%; Score 10; DB 17; Length 26;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRCWGWYYY 10
Db      26 RRCWGWYYY 17

RESULT 45
US-09-816-763-139
; Sequence 139, Application US/09816763
; Patent No. US200201108141
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-139

Query Match      100.0%; Score 10; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRCWGWYYY 10
Db      27 RRCWGWYYY 18

RESULT 46
US-09-816-763-139/c
; Sequence 139, Application US/09816763
; Patent No. US200201108141
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc_feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-139

Query Match      100.0%; Score 10; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRCWGWYYY 10
Db      27 RRCWGWYYY 18

RESULT 47
US-10-821-568-139
; Sequence 139, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc_feature
US-10-821-568-139
```



```
; LOCATION: (1)...(27)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-139

Query Match      100.0%; Score 10; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      18 RRRCWGYY 27

RESULT 48
US-10-821-568-139/c
; Sequence 139, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 139
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(27)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-139

Query Match      100.0%; Score 10; DB 17; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      27 RRRCWGYY 18

RESULT 49
US-09-816-763-140
; Sequence 140, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: DETECTION AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140

; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(28)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-140/c
; Sequence 140, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(28)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-140

Query Match      100.0%; Score 10; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      19 RRRCWGYY 28

RESULT 50
US-09-816-763-140/c
; Sequence 140, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 140
; LENGTH: 28
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(28)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-140

Query Match      100.0%; Score 10; DB 9; Length 28;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      28 RRRCWGYY 19

RESULT 51
US-10-821-568-140
; Sequence 140, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
```

```
/ PRIOR APPLICATION NUMBER: EP 00870057.7
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 140
/ LENGTH: 28
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(28)
/ OTHER INFORMATION: n = A,T,C or G
US-10-821-568-140

Query Match      100.0%; Score 10; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
   |||||
Db 19 RRRRCWGGYY 28

RESULT 52
US-10-821-568-140/c
/ Sequence 140, Application US/10821568
/ Publication No. US20040185497A1
/ GENERAL INFORMATION:
/ APPLICANT: Remacle, Jose
/ APPLICANT: Renard, Patricia
/ APPLICANT: Art, Muriel
/ TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
/ TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
/ FILE REFERENCE: VANW212.001DV1
/ CURRENT APPLICATION NUMBER: US/10/821,568
/ CURRENT FILING DATE: 2004-04-08
/ PRIOR APPLICATION NUMBER: US 09/816,763
/ PRIOR FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: EP 00870057.7
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 140
/ LENGTH: 28
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(28)
/ OTHER INFORMATION: n = A,T,C or G
US-10-821-568-140

Query Match      100.0%; Score 10; DB 17; Length 28;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
   |||||
Db 28 RRRRCWGGYY 19

RESULT 53
US-09-816-763-141
/ Sequence 141, Application US/09816763
/ Patent No. US20020110814A1
/ GENERAL INFORMATION:
/ APPLICANT: Remacle, Jose
/ APPLICANT: Renard, Patricia
/ APPLICANT: Art, Muriel
/ TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
/ TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
/ FILE REFERENCE: VANW212.001AUS
/ CURRENT APPLICATION NUMBER: US/09/816,763
/ CURRENT FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: EP 00870057.7
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 141
/ LENGTH: 29
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(29)
/ OTHER INFORMATION: n = A,T,C or G
US-09-816-763-141

Query Match      100.0%; Score 10; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
   |||||
Db 29 RRRRCWGGYY 20

RESULT 54
US-09-816-763-141/c
/ Sequence 141, Application US/09816763
/ Patent No. US20020110814A1
/ GENERAL INFORMATION:
/ APPLICANT: Remacle, Jose
/ APPLICANT: Renard, Patricia
/ APPLICANT: Art, Muriel
/ TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
/ TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
/ FILE REFERENCE: VANW212.001AUS
/ CURRENT APPLICATION NUMBER: US/09/816,763
/ CURRENT FILING DATE: 2001-03-23
/ PRIOR APPLICATION NUMBER: EP 00870057.7
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 141
/ LENGTH: 29
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (1)..(29)
/ OTHER INFORMATION: n = A,T,C or G
US-09-816-763-141

Query Match      100.0%; Score 10; DB 9; Length 29;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRRCWGGYY 10
   |||||
Db 29 RRRRCWGGYY 20

RESULT 55
US-10-821-568-141
/ Sequence 141, Application US/10821568
/ Publication No. US20040185497A1
```



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; SEQ ID NO 143
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P33 transcriptional factor consensus sequence
; NAME/KEY: misc.feature
; LOCATION: (1)...(31)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-143

Query Match      100.0%; Score 10; DB 9; Length 31;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      31 RRRCWGYY 22

RESULT 63
US-10-821-568-143
; Sequence 143, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc.feature
; LOCATION: (1)...(31)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-143

Query Match      100.0%; Score 10; DB 17; Length 31;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      31 RRRCWGYY 22

RESULT 64
US-10-821-568-143/c
; Sequence 143, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; PRIOR FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 143
; LENGTH: 31
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc.feature
; LOCATION: (1)...(31)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-143

Query Match      100.0%; Score 10; DB 17; Length 31;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      22 RRRCWGYY 31

RESULT 65
US-09-816-763-144
; Sequence 144, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc.feature
; LOCATION: (1)...(32)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-144

Query Match      100.0%; Score 10; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCWGYY 10
        |||||
Db      23 RRRCWGYY 32

RESULT 66
US-09-816-763-144/c
; Sequence 144, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
```

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; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANN212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)...(32)
; OTHER INFORMATION: n = A,T,C or G
US-09-816-763-144
```

```

Query Match      100.0%; Score 10; DB 9; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCCWGGYY 10
        |||
Db      32 RRRCCWGGYY 23
```

```

RESULT 67
US-10-821-568-144
; Sequence 144, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANN212.001DVI
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(32)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-144
```

```

Query Match      100.0%; Score 10; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCCWGGYY 10
        |||
Db      23 RRRCCWGGYY 32
```

```

RESULT 68
US-10-821-568-144/c
; Sequence 144, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANN212.001DVI
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 144
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(32)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-144
```

```

Query Match      100.0%; Score 10; DB 17; Length 32;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRRCCWGGYY 10
        |||
Db      32 RRRCCWGGYY 23
```

```

RESULT 69
US-10-821-568-145
; Sequence 145, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANN212.001DVI
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US/09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(33)
; OTHER INFORMATION: n = A,T,C or G
US-10-821-568-145
```

Query Match 100.0%; Score 10; DB 17; Length 33;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
| | | | | | | |
Db 24 RRCWGWYYY 33

RESULT 70

US-10-821-568-145/c
; Sequence 145, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR FILING DATE: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 33
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: consensus sequence for transcriptional factor p53
; NAME/KEY: misc feature
; LOCATION: (1)...(33)
; OTHER INFORMATION: n = A,T,C or G

US-10-821-568-145

Query Match 100.0%; Score 10; DB 17; Length 33;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
| | | | | | | |
Db 33 RRCWGWYYY 24

RESULT 71

US-09-816-763-145
; Sequence 145, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: EP 00870057.7
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)...(34)
; OTHER INFORMATION: n = A,T,C or G

US-09-816-763-145

Query Match 100.0%; Score 10; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
| | | | | | | |
Db 24 RRCWGWYYY 33

RESULT 72

US-09-816-763-145/c
; Sequence 145, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR FILING DATE: 2000-03-24
; PRIOR APPLICATION NUMBER: EP 00870057.7
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 145
; LENGTH: 34
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: P53 transcriptional factor consensus sequence
; NAME/KEY: misc feature
; LOCATION: (1)...(34)
; OTHER INFORMATION: n = A,T,C or G

US-09-816-763-145

Query Match 100.0%; Score 10; DB 9; Length 34;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRCWGWYYY 10
| | | | | | | |
Db 33 RRCWGWYYY 24

RESULT 73

US-10-017-178-5
; Sequence 5, Application US/10017178
; Publication No. US20020142287A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Hirotsuka
; APPLICANT: Moskal, Joseph R.
; TITLE OF INVENTION: High Throughput Assay to Detect Inhibitors of the MAP Kinase Path
; FILE REFERENCE: 99,123-D
; CURRENT APPLICATION NUMBER: US/10/017,178
; CURRENT FILING DATE: 2001-12-14
; PRIOR FILING DATE: 2000-12-14
; PRIOR APPLICATION NUMBER: US 60/255,548
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:

```
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-10-017-178-5

Query Match          40.0%; Score 4; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WGYG 9
   ||||
Db 6 WGYG 9

RESULT 74
US-10-017-178-5/c
; Sequence 5, Application US/10017178
; Publication No. US20020142287A1
; GENERAL INFORMATION:
; APPLICANT: Yamamoto, Hirotsuka
; APPLICANT: Moskal, Joseph R.
; TITLE OF INVENTION: High Throughput Assay to Detect Inhibitors of the MAP Kinase Path
; FILE REFERENCE: 99,123-D
; CURRENT APPLICATION NUMBER: US/10/017,178
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/255,548
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: PCR primer
US-10-017-178-5

Query Match          40.0%; Score 4; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRCW 5
   ||||
Db 9 RRCW 6

RESULT 75
US-10-636-065-212
; Sequence 212, Application US/10636065
; Publication No. US20040127694A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: LaCasse, Eric
; APPLICANT: Baird, Stephen
; APPLICANT: Holcik, Martin
; APPLICANT: Young, Sean
; TITLE OF INVENTION: Antisense IAP Nucleic Acids and Uses
; FILE REFERENCE: 07891/025005
; CURRENT APPLICATION NUMBER: US/10/636,065
; PRIOR FILING DATE: 2003-08-07
; PRIOR APPLICATION NUMBER: 09/672,717
; NUMBER OF SEQ ID NOS: 231
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 212
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: 1,17,18
; OTHER INFORMATION: Y=um
; NAME/KEY: modified_base
; LOCATION: 19
; OTHER INFORMATION: Y=cm
; FEATURE:
; OTHER INFORMATION: based on Homo sapiens
US-10-636-065-212

Query Match          40.0%; Score 4; DB 17; Length 19;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRG 4
   ||||
Db 19 RRRG 16

RESULT 77
US-10-407-897-50
; Sequence 50, Application US/10407897
; Publication No. US20040072148A1
; GENERAL INFORMATION:
; APPLICANT: Ji, Jiuping
; APPLICANT: Manak, Mark
; APPLICANT: Gonzalez, Irene
; TITLE OF INVENTION: Simultaneous Detection of HBV, HCV, and HIV in Plasma Samples
; FILE REFERENCE: 1589.0280002
; CURRENT APPLICATION NUMBER: US/10/407,897
; PRIOR FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 10/130,533
; PRIOR FILING DATE: 2002-11-17
; PRIOR APPLICATION NUMBER: PCT/ US00/31738
```


; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/165,916
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Primer
US-10-407-897-50

Query Match 40.0%; Score 4; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRCW 5
Db 11 RRCW 14

RESULT 78

US-10-407-897-50/c
; Sequence 50, Application US/10407897
; Publication No. US20040072148A1
; GENERAL INFORMATION:
; APPLICANT: Ji, Jiuping
; APPLICANT: Gonzalez, Irene
; TITLE OF INVENTION: Simultaneous Detection of HBV, HCV, and HIV in Plasma Samples
; TITLE OF INVENTION: Using a Multiplex Capture Assay
; FILE REFERENCE: 1589.0280002
; CURRENT APPLICATION NUMBER: US/10/407,897
; CURRENT FILING DATE: 2003-04-07
; PRIOR APPLICATION NUMBER: 10/130,533
; PRIOR FILING DATE: 2002-11-17
; PRIOR APPLICATION NUMBER: PCT/ US00/31738
; PRIOR FILING DATE: 2000-11-17
; PRIOR APPLICATION NUMBER: US 60/165,916
; PRIOR FILING DATE: 1999-11-17
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic Oligonucleotide Primer
US-10-407-897-50

Query Match 40.0%; Score 4; DB 16; Length 21;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGYI 9
Db 14 WGYI 11

RESULT 79

US-10-225-519-16
; Sequence 16, Application US/10225519
; Publication No. US20030086940A1
; GENERAL INFORMATION:
; APPLICANT: Costa, Cristina
; APPLICANT: Pizzolato, Maryellen C.
; APPLICANT: Fodor, William L.
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CELL
; TITLE OF INVENTION: EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM
; FILE REFERENCE: 33-CIP
; CURRENT APPLICATION NUMBER: US/10/225,519
; CURRENT FILING DATE: 2002-08-20

; PRIOR APPLICATION NUMBER: US 09/928,267
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/29151
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: US 60/161,186
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' forward primer.
US-10-225-519-16

Query Match 40.0%; Score 4; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYYY 10
Db 19 GYYY 22

RESULT 80

US-10-225-519-16/c
; Sequence 16, Application US/10225519
; Publication No. US20030086940A1
; GENERAL INFORMATION:
; APPLICANT: Costa, Cristina
; APPLICANT: Pizzolato, Maryellen C.
; APPLICANT: Fodor, William L.
; TITLE OF INVENTION: AN ENGINEERED RECOMBINANT MOLECULE THAT REGULATES HUMORAL AND CELL
; TITLE OF INVENTION: EFFECTOR FUNCTIONS OF THE IMMUNE SYSTEM
; FILE REFERENCE: 33-CIP
; CURRENT APPLICATION NUMBER: US/10/225,519
; CURRENT FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: US 09/928,267
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/29151
; PRIOR FILING DATE: 2000-10-21
; PRIOR APPLICATION NUMBER: US 60/161,186
; PRIOR FILING DATE: 1999-10-22
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: 5' forward primer.
US-10-225-519-16

Query Match 40.0%; Score 4; DB 14; Length 25;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRRC 4
Db 22 RRRC 19

RESULT 81

US-09-780-651-3
; Sequence 3, Application US/09780651
; Patent No. US20020048756A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, Daniel
; APPLICANT: Kung, Hsing-Jien
; TITLE OF INVENTION: Analysis of Gene Family Expression
; FILE REFERENCE: CASE-06110
; CURRENT APPLICATION NUMBER: US/09/780,651

; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/073,407
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-780-651-3

Query Match 40.0%; Score 4; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WGGY 8
|||
Db 16 WGGY 19

RESULT 82
US-09-780-651-3/c
; Sequence 3, Application US/09780651
; Patent No. US20020048756A1
; GENERAL INFORMATION:
; APPLICANT: Robinson, Daniel
; APPLICANT: Kung, Heing-Jien
; TITLE OF INVENTION: Analysis of Gene Family Expression
; FILE REFERENCE: CASE-06110
; CURRENT APPLICATION NUMBER: US/09/780,651
; CURRENT FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 09/073,407
; PRIOR FILING DATE: 1998-05-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 3
; LENGTH: 27
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-780-651-3

Query Match 40.0%; Score 4; DB 9; Length 27;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RCWW 6
|||
Db 19 RCWW 16

RESULT 83
US-10-658-093-51
; Sequence 51, Application US/10658093
; Publication No. US20040115704A1
; GENERAL INFORMATION:
; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 51
; LENGTH: 30
; TYPE: RNA

; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are
; selected from any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or u
US-10-658-093-51

Query Match 40.0%; Score 4; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRC 4
|||
Db 21 RRRRC 24

RESULT 84
US-10-658-093-51/c
; Sequence 51, Application US/10658093
; Publication No. US20040115704A1
; GENERAL INFORMATION:
; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 51
; LENGTH: 30
; TYPE: RNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are
; selected from any nucleotide
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or u
US-10-658-093-51

Query Match 40.0%; Score 4; DB 17; Length 30;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRRRC 4
|||
Db 14 RRRRC 11

RESULT 85
US-10-658-093-52
; Sequence 52, Application US/10658093
; Publication No. US20040115704A1
; GENERAL INFORMATION:
; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09

```

; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 30
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are
; OTHER INFORMATION: selected from any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or t
US-10-658-093-52

```

```

Query Match      40.0%; Score 4; DB 17; Length 30;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RRRRC 4
      |||||
Db      21 RRRRC 24

```

```

RESULT 86
US-10-658-093-52/c
; Sequence 52, Application US/10658093
; Publication No. US20040115704A1
; GENERAL INFORMATION:
; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 30
; TYPE: DNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are
; OTHER INFORMATION: selected from any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or t
US-10-658-093-52

```

```

Query Match      40.0%; Score 4; DB 17; Length 30;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RRRRC 4
      |||||
Db      14 RRRRC 11

```

```

RESULT 87
US-10-658-093-51
; Sequence 51, Application US/10658093
; Publication No. US20040209274A2
; GENERAL INFORMATION:

```

```

; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 30
; TYPE: RNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are
; OTHER INFORMATION: selected from any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or u
US-10-658-093-51

```

```

Query Match      40.0%; Score 4; DB 18; Length 30;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RRRRC 4
      |||||
Db      21 RRRRC 24

```

```

RESULT 88
US-10-658-093-51/c
; Sequence 51, Application US/10658093
; Publication No. US20040209274A2
; GENERAL INFORMATION:
; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis
; FILE REFERENCE: 12177722
; CURRENT APPLICATION NUMBER: US/10/658,093
; CURRENT FILING DATE: 2003-09-09
; PRIOR APPLICATION NUMBER: USSN 60/274770
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: PCT/AU02/00351
; PRIOR FILING DATE: 2001-03-08
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 51
; LENGTH: 30
; TYPE: RNA
; ORGANISM: mammalian
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (4)..(4)
; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are
; OTHER INFORMATION: selected from any nucleotide
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (19)..(19)
; OTHER INFORMATION: n is a, c, g, or u
US-10-658-093-51

```

```

Query Match      40.0%; Score 4; DB 18; Length 30;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RRRRC 4
      |||||
Db      14 RRRRC 11

```

RESULT 89

US-10-658-093-52
; Sequence 52, Application US/10658093
; Publication No. US20040209274A2

GENERAL INFORMATION:

; APPLICANT: Daly, John Michael
; TITLE OF INVENTION: Constructs for Gene Expression Analysis

; FILE REFERENCE: 12177722

; CURRENT APPLICATION NUMBER: US/10/658,093

; CURRENT FILING DATE: 2003-09-09

; PRIOR APPLICATION NUMBER: USSN 60/274770

; PRIOR FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: PCT/AU02/00351

; PRIOR FILING DATE: 2001-03-08

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 52

; LENGTH: 30

; TYPE: DNA

; ORGANISM: mammalian

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (4)..(4)

; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are selected from any nucleotide

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (19)..(19)

; OTHER INFORMATION: n is a, c, g, or t

US-10-658-093-52

Query Match

Best Local Similarity 40.0%; Score 4; DB 18; Length 30;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRC 4

Db 21 RRC 24

RESULT 90

US-10-658-093-52/c

; Sequence 52, Application US/10658093

; Publication No. US20040209274A2

GENERAL INFORMATION:

; APPLICANT: Daly, John Michael

; TITLE OF INVENTION: Constructs for Gene Expression Analysis

; FILE REFERENCE: 12177722

; CURRENT APPLICATION NUMBER: US/10/658,093

; CURRENT FILING DATE: 2003-09-09

; PRIOR APPLICATION NUMBER: USSN 60/274770

; PRIOR FILING DATE: 2001-03-09

; PRIOR APPLICATION NUMBER: PCT/AU02/00351

; PRIOR FILING DATE: 2001-03-08

; NUMBER OF SEQ ID NOS: 57

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 52

; LENGTH: 30

; TYPE: DNA

; ORGANISM: mammalian

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (4)..(4)

; OTHER INFORMATION: n = from 20-40 nucleotides, wherein individual nucleotides are selected from any nucleotide

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (19)..(19)

; OTHER INFORMATION: n is a, c, g, or t

US-10-658-093-52

Query Match

Best Local Similarity 40.0%; Score 4; DB 18; Length 30;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRC 4

Db 14 RRC 11

RESULT 91

US-09-179-536B-320

; Sequence 320, Application US/09179536B

; Patent No. US20020042112A1

GENERAL INFORMATION:

; APPLICANT: Hubert K ster

; David M. Lough

; Guobing Xiang

; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY

; NUMBER OF SEQUENCES: 320

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Heller Ehrman White & McAuliffe

; STREET: 4250 Executive Square, 7th Floor

; CITY: La Jolla

; STATE: CA

; COUNTRY: USA

; ZIP: 92037

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/179,536B

; FILING DATE: 26-Oct-1998

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/US97/20444

; FILING DATE: 06-NOV-1997

; APPLICATION NUMBER: 08/947,801

; FILING DATE: 08-Oct-97

; APPLICATION NUMBER: 08/933,792

; FILING DATE: 19-Sep-97

; APPLICATION NUMBER: 08/787,639

; FILING DATE: 23-Jan-97

; APPLICATION NUMBER: 08/786,988

; FILING DATE: 23-Jan-97

; APPLICATION NUMBER: 08/746,055

; FILING DATE: 06-No. US20020042112A1-96

; APPLICATION NUMBER: 08/746,036

; FILING DATE: 06-No. US20020042112A1-96

; APPLICATION NUMBER: 08/744,590

; FILING DATE: 06-No. US20020042112A1-96

; APPLICATION NUMBER: 08/744,481

; FILING DATE: 06-No. US20020042112A1-96

; ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L.

; REGISTRATION NUMBER: 33,779

; REFERENCE/DOCKET NUMBER: 24736-2004B

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 858-450-8400

; TELEFAX: 858-587-5360

; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 320:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 38 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: unknown

; MOLECULE TYPE: cDNA

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; FRAGMENT TYPE: <Unknown>

; ORIGINAL SOURCE:

; SEQUENCE DESCRIPTION: SEQ ID NO: 320;
US-09-179-536B-320

Query Match 40.0%; Score 4; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWWG 7
| | | |
Db 33 CWWG 36

RESULT 92

US-09-179-536B-320/c
; Sequence 320, Application US/09179536B
; Patent No. US20020042112A1
; GENERAL INFORMATION:
; APPLICANT: Hubert K ster
; David M. Lough
; Guobing Xiang

; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/179,536B
; FILING DATE: 26-Oct-1998
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US97/20444
; FILING DATE: 06-NOV-1997
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-No. US20020042112A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-No. US20020042112A1-96

; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-587-5360
; TELEX: <Unknown>

; INFORMATION FOR SEQ ID NO: 320:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO

; ANTI-SENSE: NO
; FRAGMENT TYPE: <Unknown>
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 320:
US-09-179-536B-320

Query Match 40.0%; Score 4; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWWG 7
| | | |
Db 36 CWWG 33

RESULT 93

US-09-297-576A-320
; Sequence 320, Application US/09297576A
; Publication No. US20030129589A1
; GENERAL INFORMATION:
; APPLICANT: KOSTER, Hubert
; APPLICANT: LITTLE, Daniel P.
; APPLICANT: BRAUN, Andreas
; APPLICANT: LOUGH, David M.
; APPLICANT: XIANG, Guobing
; APPLICANT: VAN DEN BOOM, Dirk
; APPLICANT: JURINKE, Christian
; APPLICANT: RUPPERT, Andreas
; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
; NUMBER OF SEQUENCES: 320
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Heller Ehrman White & McAuliffe
; STREET: 4250 Executive Square, 7th Floor
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/297,576A
; FILING DATE: 07-Jun-2000
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/947,801
; FILING DATE: 08-Oct-97
; APPLICATION NUMBER: 08/933,792
; FILING DATE: 19-Sep-97
; APPLICATION NUMBER: 08/787,639
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/786,988
; FILING DATE: 23-Jan-97
; APPLICATION NUMBER: 08/746,055
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/746,036
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,590
; FILING DATE: 06-No. US20030129589A1-96
; APPLICATION NUMBER: 08/744,481
; FILING DATE: 06-No. US20030129589A1-96

; ATTORNEY/AGENT INFORMATION:
; NAME: Seidman, Stephanie L
; REGISTRATION NUMBER: 33,779
; REFERENCE/DOCKET NUMBER: 24736-2004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 858-450-8400
; TELEFAX: 858-450-8499
; INFORMATION FOR SEQ ID NO: 320:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 38 base pairs

; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: CDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: <Unknown>
 ; ORIGINAL SOURCE:
 US-09-297-576A-320

Query Match 40.0%; Score 4; DB 10; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWG 7
 Db 33 CWG 36

RESULT 94

US-09-297-576A-320/c
 ; Sequence 320, Application US/09297576A
 ; Publication No. US20030129589A1

GENERAL INFORMATION:

; APPLICANT: KOSTER, Hubert
 ; APPLICANT: LITTLE, Daniel P.
 ; APPLICANT: BRAUN, Andreas
 ; APPLICANT: LOUGH, David M.
 ; APPLICANT: XIANG, Guobing
 ; APPLICANT: VAN DEN BOOM, Dirk
 ; APPLICANT: JURINKE, Christian
 ; APPLICANT: RUPPERT, Andreas
 ; TITLE OF INVENTION: DNA DIAGNOSTICS BASED ON MASS SPECTROMETRY
 ; NUMBER OF SEQUENCES: 320

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Heller Ehrman White & McAuliffe
 ; STREET: 4250 Executive Square, 7th Floor
 ; CITY: La Jolla
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 92037

COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS
 ; SOFTWARE: ASCII

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/297,576A
 ; FILING DATE: 07-Jun-2000

CLASSIFICATION:

; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/947,801
 ; FILING DATE: 08-Oct-97
 ; APPLICATION NUMBER: 08/933,792
 ; FILING DATE: 19-Sep-97
 ; APPLICATION NUMBER: 08/787,639
 ; FILING DATE: 23-Jan-97
 ; APPLICATION NUMBER: 08/786,988
 ; FILING DATE: 23-Jan-97
 ; APPLICATION NUMBER: 08/746,055
 ; FILING DATE: 06-No. US20030129589A1-96
 ; APPLICATION NUMBER: 08/746,036
 ; FILING DATE: 06-No. US20030129589A1-96
 ; APPLICATION NUMBER: 08/744,590
 ; FILING DATE: 06-No. US20030129589A1-96
 ; APPLICATION NUMBER: 08/744,481
 ; FILING DATE: 06-No. US20030129589A1-96

ATTORNEY/AGENT INFORMATION:

; NAME: Seidman, Stephanie L.
 ; REGISTRATION NUMBER: 33,779
 ; REFERENCE/DOCKET NUMBER: 24736-2004
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 858-450-8400

; TELEFAX: 858-450-8499
 ; INFORMATION FOR SEQ ID NO: 320:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 38 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: CDNA
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE: <Unknown>
 ; ORIGINAL SOURCE:
 US-09-297-576A-320

Query Match 40.0%; Score 4; DB 10; Length 38;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWG 7
 Db 36 CWG 33

RESULT 95

US-10-293-252C-5
 ; Sequence 5, Application US/10293252C
 ; Publication No. US20040103449A1

GENERAL INFORMATION:

; APPLICANT: Xu, Dongmei
 ; TITLE OF INVENTION: Identification and Use of Cytochrome
 ; FILE REFERENCE: 78127
 ; CURRENT APPLICATION NUMBER: US/10/293,252C
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: 60/363,684
 ; PRIOR FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/347,444
 ; PRIOR FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: 60/337,684
 ; PRIOR FILING DATE: 2001-11-13
 ; NUMBER OF SEQ ID NOS: 152
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 5
 ; LENGTH: 4
 ; TYPE: DNA
 ; ORGANISM: Nicotiana

US-10-293-252C-5

Query Match 30.0%; Score 3; DB 17; Length 4;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
 Db 2 RRC 4

RESULT 96

US-10-293-252C-5/c
 ; Sequence 5, Application US/10293252C
 ; Publication No. US20040103449A1

GENERAL INFORMATION:

; APPLICANT: Xu, Dongmei
 ; TITLE OF INVENTION: Identification and Use of Cytochrome
 ; FILE REFERENCE: 78127
 ; CURRENT APPLICATION NUMBER: US/10/293,252C
 ; CURRENT FILING DATE: 2002-11-13
 ; PRIOR APPLICATION NUMBER: 60/363,684
 ; PRIOR FILING DATE: 2002-03-12
 ; PRIOR APPLICATION NUMBER: 60/347,444
 ; PRIOR FILING DATE: 2002-01-11
 ; PRIOR APPLICATION NUMBER: 60/337,684

; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 152
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Nicotiana
US-10-293-252C-5

Query Match 30.0%; Score 3; DB 17; Length 4;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9
|||
Db 4 GY 2

RESULT 97
US-10-340-861B-5
; Sequence 5, Application US/10340861B
; Publication No. US20040111759A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Identification and Use of Cytochrome
; FILE REFERENCE: 78406
; CURRENT APPLICATION NUMBER: US/10/340,861B
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 10/293,252
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/363,684
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/347,444
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 60/337,684
; PRIOR FILING DATE: 2001-11-13
; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Nicotiana
US-10-340-861B-5

Query Match 30.0%; Score 3; DB 17; Length 4;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 2 RRC 4

RESULT 98
US-10-340-861B-5/c
; Sequence 5, Application US/10340861B
; Publication No. US20040111759A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Dongmei
; TITLE OF INVENTION: Identification and Use of Cytochrome
; FILE REFERENCE: 78406
; CURRENT APPLICATION NUMBER: US/10/340,861B
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 10/293,252
; PRIOR FILING DATE: 2002-11-13
; PRIOR APPLICATION NUMBER: 60/363,684
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: 60/347,444
; PRIOR FILING DATE: 2002-01-11
; PRIOR APPLICATION NUMBER: 60/337,684
; PRIOR FILING DATE: 2001-11-13

; NUMBER OF SEQ ID NOS: 184
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 4
; TYPE: DNA
; ORGANISM: Nicotiana
US-10-340-861B-5

Query Match 30.0%; Score 3; DB 17; Length 4;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9
|||
Db 4 GY 2

RESULT 99
US-10-253-117-1
; Sequence 1, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-1

Query Match 30.0%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 1 RRC 3

RESULT 100
US-10-253-117-1/c
; Sequence 1, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-1

Query Match 30.0%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4

```
Db          |||
            6 RRC 4

RESULT 101
US-10-253-117-2
; Sequence 2, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-2

Query Match          30.0%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          7 GY 9
            |||
Db          4 GY 6

RESULT 102
US-10-253-117-2/c
; Sequence 2, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 6
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-2

Query Match          30.0%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 RRC 4
            |||
Db          6 RRC 4

RESULT 103
US-10-290-545-27
; Sequence 27, Application US/10290545
; Publication No. US20030125292A1
; GENERAL INFORMATION:
; APPLICANT: Klimuk, Sean
; APPLICANT: Klimuk, Sandy
; APPLICANT: Yuan, Zuan-Ning
; TITLE OF INVENTION: IMPROVED MUCOSEAL VACCINES AND METHODS FOR USING THE SAME
; FILE REFERENCE: A-71854/TAL/AXG
; CURRENT APPLICATION NUMBER: US/10/290,545
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-290-545-27

Query Match          30.0%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 RRC 4
            |||
Db          6 RRC 4

RESULT 104
US-10-290-545-27/c
; Sequence 27, Application US/10290545
; Publication No. US20030125292A1
; GENERAL INFORMATION:
; APPLICANT: Klimuk, Sean
; APPLICANT: Klimuk, Sandy
; APPLICANT: Yuan, Zuan-Ning
; TITLE OF INVENTION: IMPROVED MUCOSEAL VACCINES AND METHODS FOR USING THE SAME
; FILE REFERENCE: A-71854/TAL/AXG
; CURRENT APPLICATION NUMBER: US/10/290,545
; CURRENT FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-290-545-27

Query Match          30.0%; Score 3; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY          2 RRC 4
            |||
Db          6 RRC 4

RESULT 105
US-10-437-263-27
; Sequence 27, Application US/10437263
; Publication No. US20040009943A1
; GENERAL INFORMATION:
; APPLICANT: Simple, Sean
; APPLICANT: Tam, Ying K.
; APPLICANT: Chikh, Ghania
; APPLICANT: Hope, Michael J.
; TITLE OF INVENTION: PATHOGEN VACCINES AND METHODS FOR USING THE SAME
; FILE REFERENCE: A-72216/TAL
; CURRENT APPLICATION NUMBER: US/10/437,263
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/454,298
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 34
```


; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-437-263-27

Query Match 30.0%; Score 3; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
|||
Db 1 RRC 3

RESULT 106

US-10-437-263-27/c
; Sequence 27, Application US/10437263
; Publication No. US20040009943A1
; GENERAL INFORMATION:
; APPLICANT: Semple, Sean
; APPLICANT: Tam, Ying K.
; APPLICANT: Klimuk, Sandra
; APPLICANT: Chikh, Ghania
; APPLICANT: Hope, Michael J.
; TITLE OF INVENTION: PATHOGEN VACCINES AND METHODS FOR USING THE SAME
; FILE REFERENCE: A-72216/TAL
; CURRENT APPLICATION NUMBER: US/10/437,263
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 60/454,298
; PRIOR FILING DATE: 2003-03-12
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-437-263-27

Query Match 30.0%; Score 3; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
|||
Db 6 RRC 4

RESULT 107

US-10-437-275-27
; Sequence 27, Application US/10437275
; Publication No. US20040009944A1
; GENERAL INFORMATION:
; APPLICANT: Semple, Sean
; APPLICANT: Klimuk, Sandra
; APPLICANT: Chikh, Ghania
; TITLE OF INVENTION: METHYLATED IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND METHODS OF
; FILE REFERENCE: A-72158/TAL
; CURRENT APPLICATION NUMBER: US/10/437,275
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646

; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/290,545
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-437-275-27

Query Match 30.0%; Score 3; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
|||
Db 1 RRC 3

RESULT 108

US-10-437-275-27/c
; Sequence 27, Application US/10437275
; Publication No. US20040009944A1
; GENERAL INFORMATION:
; APPLICANT: Tam, Ying K.
; APPLICANT: Semple, Sean
; APPLICANT: Klimuk, Sandra
; APPLICANT: Chikh, Ghania
; TITLE OF INVENTION: METHYLATED IMMUNOSTIMULATORY OLIGONUCLEOTIDES AND METHODS OF
; FILE REFERENCE: A-72158/TAL
; CURRENT APPLICATION NUMBER: US/10/437,275
; CURRENT FILING DATE: 2003-05-12
; PRIOR APPLICATION NUMBER: 60/379,343
; PRIOR FILING DATE: 2002-05-10
; PRIOR APPLICATION NUMBER: 60/460,646
; PRIOR FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: 10/290,545
; PRIOR FILING DATE: 2002-11-07
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 27
; LENGTH: 6
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: synthetic
US-10-437-275-27

Query Match 30.0%; Score 3; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
|||
Db 6 RRC 4

RESULT 109

US-10-437-258-27
; Sequence 27, Application US/10437258
; Publication No. US20040013649A1
; GENERAL INFORMATION:
; APPLICANT: Tam, Ying K.
; APPLICANT: Semple, Sean
; APPLICANT: Klimuk, Sandra
; APPLICANT: Chikh, Ghania
; TITLE OF INVENTION: CANCER VACCINES AND METHODS OF USING THE SAME
; FILE REFERENCE: A-72252/TAL
; CURRENT APPLICATION NUMBER: US/10/437,258

; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: Ets-1
US-09-816-763-32

Query Match 30.0%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WGY 8
|||
Db 6 WGY 8

RESULT 114
US-09-816-763-32/c
; Sequence 32, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art. Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: Ets-1
US-09-816-763-32

Query Match 30.0%; Score 3; DB 9; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RCW 5
|||
Db 8 RCW 6

RESULT 115
US-09-798-883B-56
; Sequence 56, Application US/09798883B
; Publication No. US20030159159A1
; GENERAL INFORMATION:
; APPLICANT: LINNIK, Matthew
; APPLICANT: RACKE, Margaret
; APPLICANT: KRAKOWSKY, Joan
; APPLICANT: SUBRAMANIAM, Arun
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and Exon 3 Promoters
; FILE REFERENCE: HMR2002C US DIV

; CURRENT APPLICATION NUMBER: US/09/798,883B
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Binding Motif in Human Nerve Growth Factor Exon 1 and 3
; OTHER INFORMATION: Promoter
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: w=a or t
US-09-798-883B-56

Query Match 30.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WGW 7
|||
Db 6 WGW 8

RESULT 116
US-09-798-883B-56/c
; Sequence 56, Application US/09798883B
; Publication No. US20030159159A1
; GENERAL INFORMATION:
; APPLICANT: LINNIK, Matthew
; APPLICANT: RACKE, Margaret
; APPLICANT: KRAKOWSKY, Joan
; APPLICANT: SUBRAMANIAM, Arun
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and Exon 3 Promoters
; FILE REFERENCE: HMR2002C US DIV
; CURRENT APPLICATION NUMBER: US/09/798,883B
; CURRENT FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 56
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Binding Motif in Human Nerve Growth Factor Exon 1 and 3
; OTHER INFORMATION: Promoter
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: w=a or t
US-09-798-883B-56

Query Match 30.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CWW 6
|||
Db 8 CWW 6

RESULT 117
US-09-326-885-56
; Sequence 56, Application US/09326885
; Publication No. US20030192065A1
; GENERAL INFORMATION:
; APPLICANT: Linnik, Matthew D
; APPLICANT: Racke, Margaret M
; APPLICANT: Krakowsky, Joan M
; APPLICANT: Subramaniam, Arun
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and
; NUMBER OF SEQUENCES: 84
; Exon 3 Promoters

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Hoechst Marion Roussel, Inc.
/ STREET: 2110 East Galbraith Road, P.O. Box 156300
/ CITY: Cincinnati
/ STATE: Ohio
/ COUNTRY: United States of America
/ ZIP: 45215-6300
/
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/326,885
/ FILING DATE: 07-Jun-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/020,179
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 60/038,212
/ FILING DATE: 06-FEB-1997
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Payne, T. Helen
/ REGISTRATION NUMBER: 36,889
/ REFERENCE/DOCKET NUMBER: HMR2002A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 513 948-7183
/ TELEFAX: 513 948-7961/4681
/ TELEX: 214320
/
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-326-885-56

Query Match 30.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 WVG 7
Db 6 WVG 8

RESULT 118
US-09-326-885-56/c
; Sequence 56, Application US/09126885
; Publication No. US20030192065A1
; GENERAL INFORMATION:
; APPLICANT: Linnik, Matthew D
; Racke, Margaret M
; Krakowsky, Joan M
; Subramaniam, Arun
;
; TITLE OF INVENTION: Human Nerve Growth Factor Exon 1 and
;
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoechst Marion Roussel, Inc.
; STREET: 2110 East Galbraith Road, P.O. Box 156300
; CITY: Cincinnati
; STATE: Ohio
; COUNTRY: United States of America
; ZIP: 45215-6300
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
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/
/ APPLICATION NUMBER: US/09/326,885
/ FILING DATE: 07-Jun-1999
/ CLASSIFICATION: <Unknown>
/
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/020,179
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 60/038,212
/ FILING DATE: 06-FEB-1997
/
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Payne, T. Helen
/ REGISTRATION NUMBER: 36,889
/ REFERENCE/DOCKET NUMBER: HMR2002A
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 513 948-7183
/ TELEFAX: 513 948-7961/4681
/ TELEX: 214320
/
/ INFORMATION FOR SEQ ID NO: 56:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: double
/ TOPOLOGY: unknown
/ MOLECULE TYPE: DNA (genomic)
/ SEQUENCE DESCRIPTION: SEQ ID NO: 56:
US-09-326-885-56

Query Match 30.0%; Score 3; DB 10; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 CWV 6
Db 8 CWV 6

RESULT 119
US-10-253-117-3
; Sequence 3, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
;
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
;
; FILE REFERENCE: 30448.6AUS01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR FILING DATE: 1999-07-02
;
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-3

Query Match 30.0%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RRC 4
Db 1 RRC 3

RESULT 120
US-10-253-117-3/c
; Sequence 3, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eyal R.
; APPLICANT: KOBAYASHI, Hiroko
;
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
```

```
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-3

Query Match      30.0%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RRC 4
DB      6 RRC 4

RESULT 121
US-10-821-568-32
; Sequence 32, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANW212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: Ets-1
US-10-821-568-32

Query Match      30.0%; Score 3; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WGY 8
DB      6 WGY 8

RESULT 124
US-10-821-568-32/c
; Sequence 32, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANW212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 8
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: Ets-1
```

```
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-3

Query Match      30.0%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 RRC 4
DB      6 RRC 4

RESULT 121
US-10-253-117-4
; Sequence 4, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eval R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-4

Query Match      30.0%; Score 3; DB 15; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GYY 9
DB      4 GYY 6

RESULT 122
US-10-253-117-4/c
; Sequence 4, Application US/10253117
; Publication No. US20030119773A1
; GENERAL INFORMATION:
; APPLICANT: RAZ, Eval R.
; APPLICANT: KOBAYASHI, Hiroko
; TITLE OF INVENTION: METHOD FOR ENHANCING AN IMMUNE RESPONSE
; FILE REFERENCE: 30448.64US01
; CURRENT APPLICATION NUMBER: US/10/253,117
; CURRENT FILING DATE: 2002-09-23
; PRIOR APPLICATION NUMBER: US/09/347,343
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 8
; TYPE: DNA
; ORGANISM: synthetic oligonucleotide
US-10-253-117-4
```

OTHER INFORMATION: Ets-1
US-10-821-568-32

Query Match 30.0%; Score 3; DB 17; Length 8;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RCW 5
Db 8 RCW 6

RESULT 125

US-09-772-719-23
; Sequence 23, Application US/09772719
; Patent No. US20020137910A1

GENERAL INFORMATION:

APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/772,719
FILING DATE: 30-JAN-2001
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.

REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3E
TELEPHONE: 415-981-2034
TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:
LENGTH: 10 base pairs
TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

DESCRIPTION: Initiator consensus sequence

US-09-772-719-23

Query Match 30.0%; Score 3; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 1 YYY 3

RESULT 126

US-09-772-719-23/C
; Sequence 23, Application US/09772719
; Patent No. US20020137910A1

GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/772,719
FILING DATE: 30-JAN-2001
CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/485,049
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.

REGISTRATION NUMBER: 30,863

REFERENCE/DOCKET NUMBER: D-0021.3E

TELEPHONE: 415-981-2034

TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 23:

SEQUENCE CHARACTERISTICS:

LENGTH: 10 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

DESCRIPTION: Initiator consensus sequence

US-09-772-719-23

Query Match 30.0%; Score 3; DB 9; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 10 RRR 8

RESULT 127

US-09-967-237-23
; Sequence 23, Application US/09967237
; Publication No. US20030049828A1

GENERAL INFORMATION:

APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
FILE REFERENCE: D-0021.5B-2
CURRENT APPLICATION NUMBER: US/09/967,237
CURRENT FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/178,115
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23

LENGTH: 10

TYPE: DNA

ORGANISM: HUMAN

```
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (3)..(8)
; OTHER INFORMATION: The letter "w" stands for a or t
US-09-967-237-23

Query Match      30.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 YYY 10
      |||
Db      1 YYY 3

RESULT 128
US-09-967-237-23/c
; Sequence 23, Application US/09967237
; Publication No. US20030049828A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; FILE REFERENCE: D-0021.5B-2
; CURRENT APPLICATION NUMBER: US/09/967,237
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 09/178,115
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 116
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 10
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
US-09-967-237-23

Query Match      30.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRR 3
      |||
Db      10 RRR 8

RESULT 129
US-10-124-759-3
; Sequence 3, Application US/10124759
; Publication No. US20030055017A1
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: Draghia-Akli, Ruxandra
; APPLICANT: Li, Xuyang
; APPLICANT: Eastman, Eric
; TITLE OF INVENTION: GHRH Expression System and Methods of Use
; FILE REFERENCE: 236/006 GeneMedicine
; CURRENT APPLICATION NUMBER: US/10/124,759
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US/09/122,171
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 60/053,609
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
US-10-124-759-3

Query Match      30.0%; Score 3; DB 10; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 RRR 3
      |||
Db      10 RRR 8

RESULT 129
US-10-124-759-3
; Sequence 3, Application US/10124759
; Publication No. US20030055017A1
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: Draghia-Akli, Ruxandra
; APPLICANT: Li, Xuyang
; APPLICANT: Eastman, Eric
; TITLE OF INVENTION: GHRH Expression System and Methods of Use
; FILE REFERENCE: 236/006 GeneMedicine
; CURRENT APPLICATION NUMBER: US/10/124,759
; CURRENT FILING DATE: 2002-04-16
; PRIOR APPLICATION NUMBER: US/09/122,171
; PRIOR FILING DATE: 1998-07-24
; PRIOR APPLICATION NUMBER: 60/053,609
; PRIOR FILING DATE: 1997-07-24
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(10)
US-10-124-759-3

Query Match      30.0%; Score 3; DB 14; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CWw 6
      |||
Db      9 CWw 7

RESULT 131
US-10-338-587A-14
; Sequence 14, Application US/10338587A
; Publication No. US20040005319A1
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF SOUTH FLORIDA
; APPLICANT: GROTEENDORST, Gary R.
; APPLICANT: BRADHAM, Douglas M.
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; FILE REFERENCE: USF100-15
; CURRENT APPLICATION NUMBER: US/10/338,587A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 09/054,363
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: US 08/459,717
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/386,680
; PRIOR FILING DATE: 1995-02-10
```

```

; PRIOR APPLICATION NUMBER: US 08/167,628
; PRIOR FILING DATE: 1993-12-14
; PRIOR APPLICATION NUMBER: US 07/752,427
; PRIOR FILING DATE: 1991-08-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Serum response element
US-10-338-587A-14

```

```

Query Match          30.0%; Score 3; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 CW 6
      |||
Db      2 CW 4

```

RESULT 132

```

US-10-338-587A-14/c
; Sequence 14, Application US/10338587A
; Publication No. US20040005319A1
; GENERAL INFORMATION:
; APPLICANT: THE UNIVERSITY OF SOUTH FLORIDA
; APPLICANT: GROTEENDORST, Gary R.
; APPLICANT: BRADSHAW, Douglass M.
; TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR
; FILE REFERENCE: USF1100-15
; CURRENT APPLICATION NUMBER: US/10/338,587A
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: US 09/054,363
; PRIOR FILING DATE: 1998-04-02
; PRIOR APPLICATION NUMBER: US 08/459,717
; PRIOR FILING DATE: 1995-06-02
; PRIOR APPLICATION NUMBER: US 08/386,680
; PRIOR FILING DATE: 1995-02-10
; PRIOR APPLICATION NUMBER: US 08/167,628
; PRIOR FILING DATE: 1993-12-14
; PRIOR APPLICATION NUMBER: US 07/752,427
; PRIOR FILING DATE: 1991-08-30
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Serum response element
US-10-338-587A-14

```

```

Query Match          30.0%; Score 3; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 CW 6
      |||
Db      9 CW 7

```

RESULT 133

```

US-10-172-526-15
; Sequence 15, Application US/10172526
; Publication No. US20040006783A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Zhenbiao
; APPLICANT: Bailey-Serres, Julia
; APPLICANT: Baxter-Burrell, Airica
; APPLICANT: Wu, Guang

```

```

; APPLICANT: Vernoud, Vanessa
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Compositions and Methods for Modulating RopGTPase
; TITLE OF INVENTION: Activity in Plants
; FILE REFERENCE: 023070-126000US
; CURRENT APPLICATION NUMBER: US/10/172,526
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:antioxidant
; OTHER INFORMATION: response element (ARE) consensus sequence
US-10-172-526-15

```

```

Query Match          30.0%; Score 3; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 WW 7
      |||
Db      7 WW 9

```

RESULT 134

```

US-10-172-526-15/c
; Sequence 15, Application US/10172526
; Publication No. US20040006783A1
; GENERAL INFORMATION:
; APPLICANT: Yang, Zhenbiao
; APPLICANT: Bailey-Serres, Julia
; APPLICANT: Baxter-Burrell, Airica
; APPLICANT: Wu, Guang
; APPLICANT: Vernoud, Vanessa
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Compositions and Methods for Modulating RopGTPase
; TITLE OF INVENTION: Activity in Plants
; FILE REFERENCE: 023070-126000US
; CURRENT APPLICATION NUMBER: US/10/172,526
; CURRENT FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:antioxidant
; OTHER INFORMATION: response element (ARE) consensus sequence
US-10-172-526-15

```

```

Query Match          30.0%; Score 3; DB 16; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 CW 6
      |||
Db      9 CW 7

```

RESULT 135

```

US-10-689-006-32
; Sequence 32, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72

```


;
; CURRENT APPLICATION NUMBER: US/10/689,006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Serine-glycine-poly-tyrosine linking peptide
US-10-689-006-32

Query Match 30.0%; Score 3; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 6 YYY 8

RESULT 136
US-10-689-006-32/c
; Sequence 32, Application US/10689006
; Publication No. US20040191249A1
; GENERAL INFORMATION:
; APPLICANT: Vanderbilt University
; APPLICANT: Hallahan, Dennis E
; APPLICANT: Mernaugh, Raymond
; TITLE OF INVENTION: PHAGE ANTIBODIES TO RADIATION-INDUCIBLE NEOANTIGENS
; FILE REFERENCE: 1242/72
; CURRENT APPLICATION NUMBER: US/10/689,006
; CURRENT FILING DATE: 2003-10-20
; PRIOR APPLICATION NUMBER: US 09/914,605
; PRIOR FILING DATE: 2001-08-30
; PRIOR APPLICATION NUMBER: US 10/259,087
; PRIOR FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 10
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Serine-glycine-poly-tyrosine linking peptide
US-10-689-006-32

Query Match 30.0%; Score 3; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 10 RRR 8

RESULT 137
US-10-888-694-23
; Sequence 23, Application US/10888694
; Publication No. US20050003425A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 465 California Street, Suite 450

;
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/888,694
; FILING DATE: 08-Jul-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719
; FILING DATE: 30-Jan-2001
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3A-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-888-694-23

Query Match 30.0%; Score 3; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 1 YYY 3

RESULT 138
US-10-888-694-23/c
; Sequence 23, Application US/10888694
; Publication No. US20050003425A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 465 California Street, Suite 450
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/888,694
; FILING DATE: 08-Jul-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719

```

; FILING DATE: 30-Jan-2001
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3A-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 23:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; DESCRIPTION: Initiator consensus sequence
; SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-10-888-694-23

Query Match          30.0%; Score 3; DB 18; Length 10;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 10 RRR 8

RESULT 139
US-10-359-050-3
; Sequence 3, Application US/10359050
; Publication No. US20030186291A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS DEUTSCHLAND GMBH
; TITLE OF INVENTION: GENETICALLY ENGINEERED PHIC31-INTEGRASE GENES
; FILE REFERENCE: AR03-001
; CURRENT APPLICATION NUMBER: US/10/359,050
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/354,741
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Splice acceptor sequence
; NAME/KEY: misc.feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-3

Query Match          30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 140
US-10-359-050-3/c
; Sequence 3, Application US/10359050
; Publication No. US20030186291A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS DEUTSCHLAND GMBH
; TITLE OF INVENTION: GENETICALLY ENGINEERED PHIC31-INTEGRASE GENES
; FILE REFERENCE: AR03-001
; CURRENT APPLICATION NUMBER: US/10/359,050
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/354,741
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Splice acceptor site.
; NAME/KEY: misc.feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-4

Query Match          30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 142
US-10-359-050-4/c
; Sequence 4, Application US/10359050
; Publication No. US20030186291A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS DEUTSCHLAND GMBH
; TITLE OF INVENTION: GENETICALLY ENGINEERED PHIC31-INTEGRASE GENES
; FILE REFERENCE: AR03-001
; CURRENT APPLICATION NUMBER: US/10/359,050
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/354,741
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Splice acceptor site.
; NAME/KEY: misc.feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-4

```

```

; CURRENT APPLICATION NUMBER: US/10/359,050
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/354,741
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Splice acceptor sequence
; NAME/KEY: misc.feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-3

Query Match          30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
Db 7 RRR 5

RESULT 141
US-10-359-050-4
; Sequence 4, Application US/10359050
; Publication No. US20030186291A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS DEUTSCHLAND GMBH
; TITLE OF INVENTION: GENETICALLY ENGINEERED PHIC31-INTEGRASE GENES
; FILE REFERENCE: AR03-001
; CURRENT APPLICATION NUMBER: US/10/359,050
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/354,741
; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Splice acceptor site.
; NAME/KEY: misc.feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-4

Query Match          30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
Db 1 YYY 3

RESULT 142
US-10-359-050-4/c
; Sequence 4, Application US/10359050
; Publication No. US20030186291A1
; GENERAL INFORMATION:
; APPLICANT: EXELIXIS DEUTSCHLAND GMBH
; TITLE OF INVENTION: GENETICALLY ENGINEERED PHIC31-INTEGRASE GENES
; FILE REFERENCE: AR03-001
; CURRENT APPLICATION NUMBER: US/10/359,050
; CURRENT FILING DATE: 2003-02-05
; PRIOR APPLICATION NUMBER: US 60/354,741

```

; PRIOR FILING DATE: 2002-02-06
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Splice acceptor site.
; NAME/KEY: misc_feature
; LOCATION: (1)..(12)
; OTHER INFORMATION: Y is T or C; N is A, C, G, or T.
US-10-359-050-4

Query Match 30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
|||
Db 7 RRR 5

RESULT 143
US-10-300-011-78
; Sequence 78, Application US/10300011
; Publication No. US20030235890A1
; GENERAL INFORMATION:
; APPLICANT: WYLLIE, DAVID
; APPLICANT: DUFF, GORDON W.
; APPLICANT: AZIZ, NAZNEEN
; APPLICANT: HSIEH, CHUNG MING
; APPLICANT: KORNMAN, KENNETH S.
; TITLE OF INVENTION: FUNCTIONAL POLYMORPHISMS OF THE INTERLEUKIN-1 LOCUS
; TITLE OF INVENTION: AFFECTING TRANSCRIPTION AND SUSCEPTIBILITY TO
; FILE REFERENCE: MSA-024.01
; CURRENT APPLICATION NUMBER: US/10/300,011
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: consensus sequence
; NAME/KEY: modified_base
; LOCATION: (6)
; OTHER INFORMATION: a, t, c or g
US-10-300-011-78

Query Match 30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
|||
Db 7 YYY 9

RESULT 144
US-10-300-011-78/c
; Sequence 78, Application US/10300011
; Publication No. US20030235890A1
; GENERAL INFORMATION:
; APPLICANT: WYLLIE, DAVID
; APPLICANT: DUFF, GORDON W.
; APPLICANT: AZIZ, NAZNEEN
; APPLICANT: HSIEH, CHUNG MING

; APPLICANT: KORNMAN, KENNETH S.
; TITLE OF INVENTION: FUNCTIONAL POLYMORPHISMS OF THE INTERLEUKIN-1 LOCUS
; TITLE OF INVENTION: AFFECTING TRANSCRIPTION AND SUSCEPTIBILITY TO
; FILE REFERENCE: MSA-024.01
; CURRENT APPLICATION NUMBER: US/10/300,011
; CURRENT FILING DATE: 2002-11-19
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 12
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: consensus sequence
; NAME/KEY: modified_base
; LOCATION: (6)
; OTHER INFORMATION: a, t, c or g
US-10-300-011-78

Query Match 30.0%; Score 3; DB 15; Length 12;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
|||
Db 9 RRR 7

RESULT 145
US-09-816-763-67
; Sequence 67, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: MBF-1
US-09-816-763-67

Query Match 30.0%; Score 3; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
|||
Db 11 YYY 13

RESULT 146
US-09-816-763-67/c
; Sequence 67, Application US/09816763
; Patent No. US20020110814A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose

```

; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001AUS
; CURRENT APPLICATION NUMBER: US/09/816,763
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: MBF-1
US-09-816-763-67

```

```

Query Match      30.0%; Score 3; DB 9; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 RRR 3
      |||
Db     13 RRR 11

```

```

RESULT 147
US-10-602-837-15
; Sequence 15, Application US/10602837
; Publication No. US20040053310A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Hua
; APPLICANT: Lis, John T.
; TITLE OF INVENTION: EXHAUSTIVE SELECTION OF RNA APTAMERS AGAINST COMPLEX
; TITLE OF INVENTION: TARGETS
; FILE REFERENCE: 19603/3921
; CURRENT APPLICATION NUMBER: US/10/602,837
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/391,255
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe

```

```

; NAME/KEY: unsure
; LOCATION: (1)..(2)
; OTHER INFORMATION: N at positions 1-2 can be A, T, G, or C
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (6)..(8)
; OTHER INFORMATION: W at positions 6-8 can be A or T
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (12)..(13)
; OTHER INFORMATION: N at positions 12-13 can be A, T, G, or C
US-10-602-837-15

```

```

Query Match      30.0%; Score 3; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      4 CWW 6
      |||
Db     5 CWW 7

```

```

RESULT 148
US-10-602-837-15/c
; Sequence 15, Application US/10602837
; Publication No. US20040053310A1
; GENERAL INFORMATION:
; APPLICANT: Shi, Hua
; APPLICANT: Lis, John T.
; TITLE OF INVENTION: EXHAUSTIVE SELECTION OF RNA APTAMERS AGAINST COMPLEX
; TITLE OF INVENTION: TARGETS
; FILE REFERENCE: 19603/3921
; CURRENT APPLICATION NUMBER: US/10/602,837
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: 60/391,255
; PRIOR FILING DATE: 2002-06-24
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Probe

```

```

; NAME/KEY: unsure
; LOCATION: (1)..(2)
; OTHER INFORMATION: N at positions 1-2 can be A, T, G, or C
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (6)..(8)
; OTHER INFORMATION: W at positions 6-8 can be A or T
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (12)..(13)
; OTHER INFORMATION: N at positions 12-13 can be A, T, G, or C
US-10-602-837-15

```

```

Query Match      30.0%; Score 3; DB 16; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      5 WWG 7
      |||
Db     7 WWG 5

```

```

RESULT 149
US-10-821-568-67
; Sequence 67, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Renard, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; FILE REFERENCE: VANM212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor

```

```
; OTHER INFORMATION: MBF-1
US-10-821-568-67

Query Match      30.0%; Score 3; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
Db      11 YYY 13

RESULT 150
US-10-821-568-67/c
; Sequence 67, Application US/10821568
; Publication No. US20040185497A1
; GENERAL INFORMATION:
; APPLICANT: Remacle, Jose
; APPLICANT: Renard, Patricia
; APPLICANT: Art, Muriel
; TITLE OF INVENTION: METHOD AND KIT FOR THE SCREENING, THE
; TITLE OF INVENTION: DETECTION AND/OR THE QUANTIFICATION OF TRANSCRIPTIONAL
; TITLE OF INVENTION: FACTORS
; FILE REFERENCE: VANW212.001DV1
; CURRENT APPLICATION NUMBER: US/10/821,568
; CURRENT FILING DATE: 2004-04-08
; PRIOR APPLICATION NUMBER: US 09/816,763
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: EP 00870057.7
; PRIOR FILING DATE: 2000-03-24
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 67
; LENGTH: 13
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence for transcriptional factor
; OTHER INFORMATION: MBF-1
US-10-821-568-67

Query Match      30.0%; Score 3; DB 17; Length 13;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
Db      13 RRR 11

RESULT 151
US-09-802-807-7
; Sequence 7, Application US/09802807
; Patent No. US2001003404A1
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michael W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: GENOMIC SEQUENCES FOR PROTEIN PRODUCTION AND DELIVERY
; FILE REFERENCE: 07236/016001
; CURRENT APPLICATION NUMBER: US/09/802,807
; CURRENT FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/084,663
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (14)
; OTHER INFORMATION: n = A,T,C or G
US-09-802-807-7

Query Match      30.0%; Score 3; DB 9; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
Db      10 RRR 8

RESULT 153
US-09-845-020A-8
; Sequence 8, Application US/09845020A
; Publication No. US20030022850A1
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michel W.
; APPLICANT: Selden, Richard F.
; TITLE OF INVENTION: Genomic Sequences for Protein Production
; TITLE OF INVENTION: and Delivery
; FILE REFERENCE: 50010/017003
; CURRENT APPLICATION NUMBER: US/09/845,020A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 09/305,384
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: US 60/084,649
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1) ... (14)
```

```
; OTHER INFORMATION: n=A,T,C or G
US-09-845-020A-8

Query Match      30.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 YYY 10
Db      1 YYY 3

RESULT 154
US-09-845-020A-8/c
; Sequence 8, Application US/09845020A
; Publication No. US20030022850A1
; GENERAL INFORMATION:
; APPLICANT: Treco, Douglas A.
; APPLICANT: Heartlein, Michel W.
; APPLICANT: Seiden, Richard F.
; TITLE OF INVENTION: Genomic Sequences for Protein Production
; TITLE OF INVENTION: and Delivery
; FILE REFERENCE: 50010/017003
; CURRENT APPLICATION NUMBER: US/09/845,020A
; CURRENT FILING DATE: 2001-04-27
; PRIOR APPLICATION NUMBER: US 09/305,384
; PRIOR FILING DATE: 1999-05-05
; PRIOR APPLICATION NUMBER: US 60/084,649
; PRIOR FILING DATE: 1998-05-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(14)
; OTHER INFORMATION: n=A,T,C or G
US-09-845-020A-8

Query Match      30.0%; Score 3; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
Db      10 RRR 8

RESULT 155
US-10-345-115-1
; Sequence 1, Application US/10345115
; Publication No. US20030224519A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, John
; APPLICANT: Jackson, Paul David
; APPLICANT: Jiang, Li
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING
; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS
; FILE REFERENCE: ATX-004CP2
; CURRENT APPLICATION NUMBER: US/10/345,115
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 10/277612
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/336497
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 10/196721
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1-10,12
; OTHER INFORMATION: n = A,T,C or G
US-10-345-115-1

Query Match      30.0%; Score 3; DB 15; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 RRR 3
Db      10 RRR 8

RESULT 157
US-10-277-612-1
; Sequence 1, Application US/10277612
; Publication No. US20040018624A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, John
; APPLICANT: Jackson, Paul David
; APPLICANT: Jiang, Li
```

;
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING
; FILE REFERENCE: ATX-004CP
; CURRENT APPLICATION NUMBER: US/10/277,612
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/336497
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 10/196721
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: 1-10;12
; OTHER INFORMATION: Y = C or T
; US-10-277-612-1

Query Match 30.0%; Score 3; DB 16; Length 14;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 1 YYY 3

RESULT 158
US-10-277-612-1/c
; Sequence 1, Application US/10277612
; Publication No. US20040018624A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, John
; APPLICANT: Jackson, Paul David
; APPLICANT: Jiang, Li
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING
; FILE REFERENCE: ATX-004CP
; CURRENT APPLICATION NUMBER: US/10/277,612
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 60/336497
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 10/196721
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n = A,T,C or G
; NAME/KEY: misc_feature
; LOCATION: 1-10;12
; OTHER INFORMATION: Y = C or T
; US-10-277-612-1

Query Match 30.0%; Score 3; DB 16; Length 14;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||

Db 10 RRR 8

RESULT 159
US-10-333-892-6
; Sequence 6, Application US/10333892
; Publication No. US20040209254A1
; GENERAL INFORMATION:
; APPLICANT: DZGenes LLC
; TITLE OF INVENTION: DIAGNOSTIC POLYMORPHISMS FOR THE TGF-BETA 1 PROMOTER
; FILE REFERENCE: DZG2185.2
; CURRENT APPLICATION NUMBER: US/10/333,892
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US 60/220,583
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US01/23368
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: n=any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (6)..(6)
; OTHER INFORMATION: SNP replaces Y with a G at this position
; US-10-333-892-6

Query Match 30.0%; Score 3; DB 18; Length 14;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 6 YYY 8

RESULT 160
US-10-333-892-6/c
; Sequence 6, Application US/10333892
; Publication No. US20040209254A1
; GENERAL INFORMATION:
; APPLICANT: DZGenes LLC
; TITLE OF INVENTION: DIAGNOSTIC POLYMORPHISMS FOR THE TGF-BETA 1 PROMOTER
; FILE REFERENCE: DZG2185.2
; CURRENT APPLICATION NUMBER: US/10/333,892
; CURRENT FILING DATE: 2003-06-24
; PRIOR APPLICATION NUMBER: US 60/220,583
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US01/23368
; PRIOR FILING DATE: 2001-07-25
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (11)..(11)
; OTHER INFORMATION: n=any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (6)..(6)
; OTHER INFORMATION: SNP replaces Y with a G at this position
; US-10-333-892-6

Query Match 30.0%; Score 3; DB 18; Length 14;

```
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 8 RRR 6

RESULT 161
US-10-342-761-1
; Sequence 1, Application US/10342761
; Publication No. US20040253727A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, John
; APPLICANT: Jackson, Paul David
; APPLICANT: Jiang, Li
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING
; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS
; FILE REFERENCE: ATX-004CPCN2
; CURRENT APPLICATION NUMBER: US/10/342,761
; CURRENT FILING DATE: 2003-01-15
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/336497
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 10/196721
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-10,12
; OTHER INFORMATION: Y = C or T
US-10-342-761-1

Query Match 30.0%; Score 3; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 10 RRR 8

RESULT 163
US-10-342-923-1
; Sequence 1, Application US/10342923
; Publication No. US20040253590A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, John
; APPLICANT: Jackson, Paul David
; APPLICANT: Jiang, Li
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING
; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS
; FILE REFERENCE: ATX-004CPCN4
; CURRENT APPLICATION NUMBER: US/10/342,923
; CURRENT FILING DATE: 2003-01-15
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 10/277612
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/336497
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-10,12
; OTHER INFORMATION: Y = C or T
US-10-342-923-1

Query Match 30.0%; Score 3; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 1 YYY 3

RESULT 164
US-10-342-923-1/c
; Sequence 1, Application US/10342923
; Publication No. US20040253590A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, John
```


; APPLICANT: Jackson, Paul David
; APPLICANT: Jiang, Li
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING
; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS
; FILE REFERENCE: ATX-004CPCN4
; CURRENT APPLICATION NUMBER: US/10/342,923
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 10/277612
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/336497
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 10/196721
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-10,12
; OTHER INFORMATION: Y = C or T
US-10-342-923-1

Query Match 30.0%; Score 3; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 10 RRR 8

RESULT 165

US-10-342-948-1
; Sequence 1, Application US/10342948
; Publication No. US20040253591A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, John
; APPLICANT: Jackson, Paul David
; APPLICANT: Jiang, Li
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING
; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS
; FILE REFERENCE: ATX-004CPCN3
; CURRENT APPLICATION NUMBER: US/10/342,948
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 10/277612
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/336497
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 10/196721
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-10,12
; OTHER INFORMATION: Y = C or T
US-10-342-948-1

Query Match 30.0%; Score 3; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YYY 10
|||
Db 1 YYY 3

RESULT 166

US-10-342-948-1/c
; Sequence 1, Application US/10342948
; Publication No. US20040253591A1
; GENERAL INFORMATION:
; APPLICANT: Harrington, John
; APPLICANT: Jackson, Paul David
; APPLICANT: Jiang, Li
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MAKING
; TITLE OF INVENTION: MUTATIONS IN CELL LINES AND ANIMALS
; FILE REFERENCE: ATX-004CPCN3
; CURRENT APPLICATION NUMBER: US/10/342,948
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 10/277612
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: 60/336497
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 10/196721
; PRIOR FILING DATE: 2002-07-15
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 11
; OTHER INFORMATION: n = A,T,C or G
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 1-10,12
; OTHER INFORMATION: Y = C or T
US-10-342-948-1

Query Match 30.0%; Score 3; DB 18; Length 14;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 RRR 3
|||
Db 10 RRR 8

RESULT 167

US-10-418-182-183
; Sequence 183, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide

US-10-418-182-183

Query Match 30.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Gaps 0;

Qy 2 RRC 4
Db 1 RRC 3

RESULT 168

US-10-418-182-183/c
; Sequence 183, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-183

Query Match 30.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9
Db 3 GY 1

RESULT 169

US-10-418-182-219
; Sequence 219, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-219

Query Match 30.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 6
Db 3 CW 5

RESULT 170

US-10-418-182-219/c
; Sequence 219, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 219
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-219

Query Match 30.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WWG 7
Db 5 WWG 3

RESULT 171

US-10-418-182-313
; Sequence 313, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-313

Query Match 30.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
Db 1 RRC 3

RESULT 172

US-10-418-182-313/c
; Sequence 313, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558

; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 313
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-313

Query Match 30.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9
|||
Db 3 GY 1

RESULT 173
US-10-418-182-421
; Sequence 421, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 421
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-421

Query Match 30.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 CW 6
|||
Db 3 CW 5

RESULT 174
US-10-418-182-421/c
; Sequence 421, Application US/10418182
; Publication No. US20030228302A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; TITLE OF INVENTION: UNIVERSAL LIBRARIES FOR IMMUNOGLOBULINS
; FILE REFERENCE: 1551.2001-001
; CURRENT APPLICATION NUMBER: US/10/418,182
; PRIOR FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,558
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 423
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 421
; LENGTH: 15
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide
US-10-418-182-421

Query Match 30.0%; Score 3; DB 15; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 WW 7
|||
Db 5 WW 3

RESULT 175
US-10-706-466-5
; Sequence 5, Application US/10706466
; Publication No. US20040082535A1
; GENERAL INFORMATION:
; APPLICANT: MAHURAN, Don J.
; APPLICANT: CLARKE, Joe T.R.
; APPLICANT: CALLAHAN, John W.
; TITLE OF INVENTION: PRODUCTS AND METHODS FOR GAUCHER DISEASE THERAPY
; FILE REFERENCE: 24,131 USA
; CURRENT APPLICATION NUMBER: US/10/706,466
; PRIOR FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/586,216
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/137,598
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 2,272,055
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc difference
; LOCATION: y=1-10; n=11
; OTHER INFORMATION: y=c or u; n=any nucleotide
US-10-706-466-5

Query Match 30.0%; Score 3; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YY 10
|||
Db 1 YY 3

RESULT 176
US-10-706-466-5/c
; Sequence 5, Application US/10706466
; Publication No. US20040082535A1
; GENERAL INFORMATION:
; APPLICANT: MAHURAN, Don J.
; APPLICANT: CLARKE, Joe T.R.
; APPLICANT: CALLAHAN, John W.
; TITLE OF INVENTION: PRODUCTS AND METHODS FOR GAUCHER DISEASE THERAPY
; FILE REFERENCE: 24,131 USA
; CURRENT APPLICATION NUMBER: US/10/706,466
; CURRENT FILING DATE: 2003-11-12
; PRIOR APPLICATION NUMBER: 09/586,216
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: 60/137,598
; PRIOR FILING DATE: 1999-06-03
; PRIOR APPLICATION NUMBER: 2,272,055
; PRIOR FILING DATE: 1999-06-02
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 5
; LENGTH: 15
; TYPE: RNA
; ORGANISM: Homo sapiens
; FEATURE:
US-10-706-466-5

; NAME/KEY: misc difference
; LOCATION: Y=1-10; n=11
; OTHER INFORMATION: Y=c or u; n=any nucleotide
US-10-706-466-5

Query Match 30.0%; Score 3; DB 16; Length 15;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 10 RRR 8

RESULT 177

US-09-754-014-11/c
; Sequence 11, Application US/09754014
; Patent No. US20020119940A1
; GENERAL INFORMATION:
; APPLICANT: Jeff No. US20020119940A1dstrom
; Bruce Freimark
; Deepa Deshpande
; TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYSTEMS
; AND USES

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/754,014
FILING DATE: 03-Jan-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/948,958
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Berkman, Charles S.
REGISTRATION NUMBER: 38,077
REFERENCE/DOCKET NUMBER: 226/284

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
OTHER INFORMATION: The letter "Y" stands for C or T.
The letter "N" stands for any base.

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-754-014-11

Query Match 30.0%; Score 3; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 YYY 10
Db 1 YYY 3

RESULT 178

US-09-754-014-11/c
; Sequence 11, Application US/09754014
; Patent No. US20020119940A1
; GENERAL INFORMATION:
; APPLICANT: Jeff No. US20020119940A1dstrom
; Bruce Freimark
; Deepa Deshpande
; TITLE OF INVENTION: GENE EXPRESSION AND DELIVERY SYSTEMS
; AND USES

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/754,014
FILING DATE: 03-Jan-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/948,958
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: Berkman, Charles S.
REGISTRATION NUMBER: 38,077
REFERENCE/DOCKET NUMBER: 226/284

TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear

FEATURE:
OTHER INFORMATION: The letter "Y" stands for C or T.
The letter "N" stands for any base.

SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-754-014-11

Query Match 30.0%; Score 3; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 RRR 3
Db 11 RRR 9

RESULT 179

US-09-836-866-7
; Sequence 7, Application US/09836866
; Patent No. US20020123473A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020123473A1dstrom, Jeff
; Freimark, Bruce
; Deshpande, Deepa

TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
DELIVERY SYSTEMS AND USES

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER READABLE FORM:
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/836,866
FILING DATE: 16-Apr-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/949,160
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 226/285
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The letter "Y" stands for C or T.
The letter "N" stands for any base.
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-836-866-7
Query Match 30.0%; Score 3; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 8 YYY 10
Db 1 YYY 3
RESULT 180
US-09-836-866-7/C
Sequence 7, Application US/09836866
Patent No. US20020123473A1
GENERAL INFORMATION:
APPLICANT: No. US20020123473A1dstrom, Jeff
Frelmark, Bruce
Deshpande, Deepa
TITLE OF INVENTION: IL-12 GENE EXPRESSION AND
DELIVERY SYSTEMS AND USES
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER READABLE FORM:
storage

COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: FastSEQ for Windows 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/836,866
FILING DATE: 16-Apr-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/949,160
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 226/285
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
OTHER INFORMATION: The letter "Y" stands for C or T.
The letter "N" stands for any base.
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-836-866-7
Query Match 30.0%; Score 3; DB 9; Length 16;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 RRR 3
Db 11 RRR 9
RESULT 181
US-09-892-867-5
Sequence 5, Application US/09892867
Patent No. US20020037568A1
GENERAL INFORMATION:
APPLICANT: MOLENAAR, DOUWE
APPLICANT: VAN DER REST, MICHEL E
APPLICANT: DRYSCH, ANDRE
TITLE OF INVENTION: NUCLEOTIDE SEQUENCE WHICH CODE FOR THE mdhA GENE
FILE REFERENCE: 203976USOX
CURRENT APPLICATION NUMBER: US/09/892,867
CURRENT FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: DE 10032350.2
PRIOR FILING DATE: 2000-07-04
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent in version 3.1
SEQ ID NO 5
LENGTH: 17
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic DNA
US-09-892-867-5
Query Match 30.0%; Score 3; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 RRC 4
Db 14 RRC 16
RESULT 182

```
US-09-892-867-5/c
; Sequence 5, Application US/09892867
; Patent No. US20020037568A1
; GENERAL INFORMATION:
; APPLICANT: MOLENAAR, DOUWE
; APPLICANT: VAN DER REST, MICHEL E
; APPLICANT: DRYSCH, ANDRE
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE WHICH CODE FOR THE mdha GENE
; FILE REFERENCE: 203976USOX
; CURRENT APPLICATION NUMBER: US/09/892,867
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: DE 10032350.2
; PRIOR FILING DATE: 2000-07-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-892-867-5

Query Match      30.0%; Score 3; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GY 9
Db      16 GY 14

RESULT 183
US-09-973-451-15
; Sequence 15, Application US/09973451
; Patent No. US20020132328A1
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AM, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/973,451
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/302,812
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,768
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 15
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Artificial Sequence
US-09-973-451-15

Query Match      30.0%; Score 3; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GY 9
Db      16 GY 14

RESULT 184
US-09-973-451-15/c
; Sequence 15, Application US/09973451
; Patent No. US20020132328A1
```

```
; GENERAL INFORMATION:
; APPLICANT: JACOBSON, Myron K.
; APPLICANT: JACOBSON, Elaine L.
; APPLICANT: AM, Jean-Christophe
; APPLICANT: LIN, Winston
; TITLE OF INVENTION: GENES ENCODING SEVERAL POLY (ADP-RIBOSE) GLYCOHYDROLASE
; TITLE OF INVENTION: (PARG) ENZYMES,
; TITLE OF INVENTION: THE PROTEINS AND FRAGMENTS THEREOF, AND ANTIBODIES IMMUNOREACTIV
; TITLE OF INVENTION: THEREWITH
; FILE REFERENCE: NIAD 201
; CURRENT APPLICATION NUMBER: US/09/973,451
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/302,812
; PRIOR FILING DATE: 1999-04-30
; PRIOR APPLICATION NUMBER: 60/083,768
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 38
; SEQ ID NO 15
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Bos taurus
; FEATURE:
; OTHER INFORMATION: Artificial Sequence
US-09-973-451-15

Query Match      30.0%; Score 3; DB 9; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 RRC 4
Db      16 RRC 14

RESULT 185
US-09-836-705-4
; Sequence 4, Application US/09836705
; Publication No. US20030078395A1
; GENERAL INFORMATION:
; APPLICANT: Abe, Yuki
; APPLICANT: Ono, Chiho
; APPLICANT: Yoshihawa, Hiroji
; TITLE OF INVENTION: Genes from a Gene Cluster
; FILE REFERENCE: 01149/HG
; CURRENT APPLICATION NUMBER: US/09/836,705
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: JP 2000-116591
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: JP 2000-117458
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Description of Artificial Sequence: A mixed primer
; OTHER INFORMATION: which has a DNA sequence deduced from the amino
; OTHER INFORMATION: acid sequence of PKS of Aspergillus flavus.
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (3)..(3)
; OTHER INFORMATION: i
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(6)
; OTHER INFORMATION: i
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: i
; FEATURE:
```

```
; NAME/KEY: modified base
; LOCATION: (15)..(15)
; OTHER INFORMATION: i
US-09-836-705-4

Query Match      30.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      3 RCW 5
      |||
Db      9 RCW 11

RESULT 186
US-09-836-705-4/c
; Sequence 4, Application US/09836705
; Publication No. US20030078395A1
; GENERAL INFORMATION:
; APPLICANT: Abe, Yuki
; APPLICANT: Ono, Chiho
; APPLICANT: Yoshikawa, Hiroji
; TITLE OF INVENTION: Genes from a Gene Cluster
; FILE REFERENCE: 01149/HG
; CURRENT APPLICATION NUMBER: US/09/836,705
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: JP 2000-116591
; PRIOR FILING DATE: 2000-04-18
; PRIOR APPLICATION NUMBER: JP 2000-117458
; PRIOR FILING DATE: 2000-04-19
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Description of Artificial Sequence: A mixed primer
; OTHER INFORMATION: which has a DNA sequence deduced from the amino
; OTHER INFORMATION: acid sequence of PKS of Aspergillus flavus.
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (3)..(3)
; OTHER INFORMATION: i
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (6)..(6)
; OTHER INFORMATION: i
; FEATURE:
; NAME/KEY: modified_base
; LOCATION: (8)..(8)
; OTHER INFORMATION: i
; FEATURE:
; NAME/KEY: modified base
; LOCATION: (15)..(15)
; OTHER INFORMATION: i
US-09-836-705-4

Query Match      30.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WGY 8
      |||
Db      11 WGY 9

RESULT 187
US-09-903-770-5
; Sequence 5, Application US/09903770
; Publication No. US20030170780A1
; GENERAL INFORMATION:
; APPLICANT: MOLENAAR, DOUWE
; APPLICANT: VAN DER REST, MICHEL E
; TITLE OF INVENTION: NUCLEOTIDE SEQUENCE WHICH CODE FOR THE mdhA GENE
; FILE REFERENCE: 203976US0X
; CURRENT APPLICATION NUMBER: US/09/903,770
; CURRENT FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: DE 10032350.2
; PRIOR FILING DATE: 2000-07-04
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic DNA
US-09-903-770-5

Query Match      30.0%; Score 3; DB 10; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GYV 9
      |||
Db      16 GYV 14

RESULT 189
US-09-876-813-10
; Sequence 10, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGPF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
```

```

; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(17)
; OTHER INFORMATION: n = A,T,C or G
US-09-876-813-10

```

```

Query Match      30.0%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 GYY 9
      |||
Db     14 GYY 16

```

```

RESULT 190
US-09-876-813-10/c
; Sequence 10, Application US/09876813
; Publication No. US20040002140A1
; GENERAL INFORMATION:
; APPLICANT: Gilbert, Teresa
; APPLICANT: Hart, Charles E.
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
; FILE REFERENCE: 99-19
; CURRENT APPLICATION NUMBER: US/09/876,813
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: US/09/564,595
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: US 09/304,216
; PRIOR FILING DATE: 1999-05-03
; PRIOR APPLICATION NUMBER: US 60/164,463
; PRIOR FILING DATE: 1999-11-10
; PRIOR APPLICATION NUMBER: US 60/180,169
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)..(17)
; OTHER INFORMATION: n = A,T,C or G
US-09-876-813-10

```

```

Query Match      30.0%; Score 3; DB 11; Length 17;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 RRC 4
      |||
Db     16 RRC 14

```

```

RESULT 191
US-10-043-142-1
; Sequence 1, Application US/10043142
; Publication No. US20020150969A1
; GENERAL INFORMATION:
; APPLICANT: DERKX, PATRICK M.F.
; APPLICANT: MADRID, SUSAN M.
; TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
; FILE REFERENCE: 078883/0128
; CURRENT APPLICATION NUMBER: US/10/043,142
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 09/806,399
; PRIOR FILING DATE: 2002-03-30
; PRIOR APPLICATION NUMBER: PCT/IB99/01669
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: GB 9821198.0
; PRIOR FILING DATE: 1998-09-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-043-142-1

```

```

Query Match      30.0%; Score 3; DB 13; Length 17;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      7 GYY 9
      |||
Db     2 GYY 4

```

```

RESULT 192
US-10-043-142-1/c
; Sequence 1, Application US/10043142
; Publication No. US20020150969A1
; GENERAL INFORMATION:
; APPLICANT: DERKX, PATRICK M.F.
; APPLICANT: MADRID, SUSAN M.
; TITLE OF INVENTION: PEPTIDYL PROLYL CIS-TRANS ISOMERASES
; FILE REFERENCE: 078883/0128
; CURRENT APPLICATION NUMBER: US/10/043,142
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: 09/806,399
; PRIOR FILING DATE: 2002-03-30
; PRIOR APPLICATION NUMBER: PCT/IB99/01669
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: GB 9821198.0
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: oligonucleotide
US-10-043-142-1

```

```

Query Match      30.0%; Score 3; DB 13; Length 17;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      2 RRC 4
      |||
Db     4 RRC 2

```


RESULT 193
US-10-139-583-10
; Sequence 10, Application US/10139583
; Publication No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G
US-10-139-583-10

Query Match 30.0%; Score 3; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GY 9
|||
Db 14 GY 16

RESULT 194
US-10-139-583-10/c
; Sequence 10, Application US/10139583
; Publication No. US20020177193A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Zeren
; APPLICANT: Hart, Charles E.
; APPLICANT: Piddington, Christopher S.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Shoemaker, Kimberly E.
; APPLICANT: Gilbertson, Debra G.
; APPLICANT: West, James W.
; TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
; FILE REFERENCE: 98-60
; CURRENT APPLICATION NUMBER: US/10/139,583
; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: 09/457,066
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 10
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide primer
; NAME/KEY: misc_feature
; LOCATION: (1)...(17)
; OTHER INFORMATION: n = A,T,C or G

US-10-139-583-10

Query Match 30.0%; Score 3; DB 13; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 RRC 4
|||
Db 16 RRC 14

RESULT 195
US-10-338-237-16
; Sequence 16, Application US/10338237
; Publication No. US20030148357A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Lok, Si
; TITLE OF INVENTION: NOVEL CYSTINE KNOT PROTEIN AND MATERIALS
; FILE REFERENCE: 97-65
; CURRENT APPLICATION NUMBER: US/10/338,237
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: US/09/250,124A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,682
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/102,709
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
; NAME/KEY: variation
; LOCATION: (1)...(17)
; OTHER INFORMATION: n is any nucleotide
US-10-338-237-16

Query Match 30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RCW 5
|||
Db 5 RCW 7

RESULT 196
US-10-338-237-16/c
; Sequence 16, Application US/10338237
; Publication No. US20030148357A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Lok, Si
; TITLE OF INVENTION: NOVEL CYSTINE KNOT PROTEIN AND MATERIALS
; FILE REFERENCE: 97-65
; CURRENT APPLICATION NUMBER: US/10/338,237
; CURRENT FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: US/09/250,124A
; PRIOR FILING DATE: 1999-02-12
; PRIOR APPLICATION NUMBER: US 60/074,682
; PRIOR FILING DATE: 1998-02-13
; PRIOR APPLICATION NUMBER: US 60/102,709
; PRIOR FILING DATE: 1998-10-01
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16

```
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
;
; NAME/KEY: variation
; LOCATION: (1)...(17)
; OTHER INFORMATION: n is any nucleotide
US-10-338-237-16

Query Match          30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 WGY 8
      |||
Db      7 WGY 5

RESULT 197
US-10-302-554-29
; Sequence 29, Application US/10302554
; Publication No. US20030148467A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4
; FILE REFERENCE: 98-59
; CURRENT APPLICATION NUMBER: US/10/302,554
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US/09/428,118
; PRIOR FILING DATE: 1999-10-27
; PRIOR APPLICATION NUMBER: US 60/105,824
; PRIOR FILING DATE: 1998-10-27
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 29
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: variation
; LOCATION: (1)...(17)
; OTHER INFORMATION: n is any nucleotide
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-10-302-554-29

Query Match          30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GY 9
      |||
Db      8 GY 10

RESULT 198
US-10-302-554-29/c
; Sequence 29, Application US/10302554
; Publication No. US20030148467A1
; GENERAL INFORMATION:
; APPLICANT: West, Robert R.
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Gao, Zeren
; TITLE OF INVENTION: INTERLEUKIN-1 HOMOLOG ZIL1A4
; FILE REFERENCE: 98-59
; CURRENT APPLICATION NUMBER: US/10/302,554
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US/09/428,118
; PRIOR FILING DATE: 1999-10-27

; LENGTH: 17
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: variation
; LOCATION: (1)...(17)
; OTHER INFORMATION: n is any nucleotide
; FEATURE:
; OTHER INFORMATION: oligonucleotide primer
US-10-302-554-29

Query Match          30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      7 GY 9
      |||
Db      8 GY 10

RESULT 199
US-10-404-300A-28
; Sequence 28, Application US/10404300A
; Publication No. US20030215856A1
; GENERAL INFORMATION:
; APPLICANT: Church, George
; APPLICANT: Bulyk, Martha
; TITLE OF INVENTION: SURFACE-BOUND, DOUBLE-STRANDED DNA PROTEIN ARRAYS
; FILE REFERENCE: 10498-00050
; CURRENT APPLICATION NUMBER: US/10/404,300A
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 09/132,368
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/061,604
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: n is a, c, g or t
US-10-404-300A-28

Query Match          30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 CW 6
      |||
Db      6 CW 8

RESULT 200
US-10-404-300A-28/c
; Sequence 28, Application US/10404300A
; Publication No. US20030215856A1
; GENERAL INFORMATION:
; APPLICANT: Church, George
; APPLICANT: Bulyk, Martha
; TITLE OF INVENTION: SURFACE-BOUND, DOUBLE-STRANDED DNA PROTEIN ARRAYS
; FILE REFERENCE: 10498-00050
; CURRENT APPLICATION NUMBER: US/10/404,300A
; CURRENT FILING DATE: 2003-04-01
; PRIOR APPLICATION NUMBER: 09/132,368
```

```
; PRIOR FILING DATE: 1998-08-11
; PRIOR APPLICATION NUMBER: 60/061,604
; PRIOR FILING DATE: 1997-10-10
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 17
; TYPE: DNA
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (9)..(9)
; OTHER INFORMATION: n is a, c, g or t
US-10-404-300A-28
```

```
Query Match      30.0%; Score 3; DB 15; Length 17;
Best Local Similarity 100.0%; Pred.No. 0;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      4 CWW 6
      |||
Db      12 CWW 10
```

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Search completed: January 14, 2005, 19:05:52
Job time : 403 secs
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